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OM protein - protein search, using sw model
Run on: July 1, 2005, 18:05:05 ; Search time 34.3148 Seconds
(without alignments)
1386.327 Million cell updates/sec

Title: US-09-591-632-2_COPY_1_123
Perfect score: 701
Sequence: 1 MSDSNQGNQNYQQYSQNG.....FNYNNLQYAGFPQPSQG 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	701	100.0	685	AAB30792	Aab30792 Amino aci
2	701	100.0	685	ABR53107	ABR53107 Protein s
3	701	100.0	685	ADK63022	ADK63022 Disease t
4	682	97.3	271	AAB30800	Aab30800 A modifie
5	450	64.2	215	AAB30799	Aab30799 A modifie
6	228	32.5	715	AAB30820	Aab30820 Amino aci
7	223	31.8	721	ABP73437	ABP73437 Candida a
8	167	23.8	592	ABO53050	ABO53050 Human put
9	167	23.8	592	ADI26209	ADI26209 Human pro
10	166	23.7	405	AAB30810	Aab30810 Amino aci
11	166	23.7	405	AAB30821	Aab30821 Amino aci
12	166	23.7	741	AAB30819	Aab30819 Amino aci
13	163.5	23.3	589	ADI26207	ADI26207 Human pro
14	163	23.3	1145	AAE09770	AAE09770 Drosophil
15	163	23.3	1145	ADB38846	ADB38846 Drosophil
16	160	22.8	407	AAE94879	AAE94879 ORF incor
17	148.5	21.2	207	ABP63118	ABP63118 FLO11 gen
18	148	21.1	417	AGS30013	AGS30013 Arabidops
19	148	21.1	419	AGS30012	AGS30012 Arabidops
20	148	21.1	439	AGS30011	AGS30011 Arabidops
21	143	20.4	518	ADI26113	ADI26113 Human pro
22	141	20.1	391	ADN03904	ADN03904 Antipsori
23	141	20.1	392	ABG10550	ABG10550 Novel hum
24	141	20.1	404	AAE90675	AAE90675 Human chr
25	141	20.1	536	AAE78356	AAE78356 Human pro

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26	139.5	19.9	492	7	ADJ69335	Adj69335 Human hea
27	139	19.8	632	8	ADN73047	Adn73047 Thale cre
28	138.5	19.8	525	5	ABG95084	Abg95084 Human tra
29	138.5	19.8	525	8	ADR14649	Adr14649 Human NF-
30	136.5	19.5	461	2	AAR75506	Aar75506 Nicotiana
31	136	19.4	462	5	ABG95083	Abg95083 Human tra
32	136	19.4	462	8	ADE77159	Ade77159 Human pro
33	136	19.4	526	4	AAW78355	Aaw78355 Human pro
34	136	19.4	526	5	ABG95081	Abg95081 Human tra
35	136	19.4	526	8	ADI26117	Adi26117 Human pro
36	136	19.4	526	8	ABM81732	Abm81732 Tumour-as
37	136	19.4	526	8	ADS88302	Ads88302 Human pro
38	135.5	19.3	345	4	ABG10551	Abg10551 Novel hum
39	135	19.3	128	4	AAE30822	Aae30822 Amino aci
40	135	19.3	128	8	ADM47991	Adm47991 Polypepti
41	134	19.1	341	2	AAE06522	Aae06522 Tapetum-s
42	134	19.1	341	2	AAE09298	Aae09298 Male flow
43	134	19.1	341	2	AAE09307	Aae09307 Male flow
44	134	19.1	341	2	AAW10628	Aaw10628 Anther-ep
45	132	18.8	437	2	AAE75507	Aae75507 Nicotiana

ALIGNMENTS

RESULT 1
AAB30792
ID AAB30792 standard; protein; 685 AA.
XX
AC AAB30792;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a yeast Sup35 protein.
XX
KW Sup35; phenotype; SCHAG; self-coalesce; higher-order aggregate;
KW amyloidogenic domain; aggregation; fibril; phenotypic alteration;
KW gene therapy; disease resistance; plant pigmentation; prion disease.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200075324-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015876.
XX
PR 09-JUN-1999; 99US-0138833P.
XX
XX (ARCH-) ARCH DEV CORP.
XX
Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel T;
WPI: 2001-061723/07.
DR N-PSDB; AAC86679.
XX
New nucleic acid encoding chimeric proteins with self-assembly
properties, useful e.g. for diagnosis and treatment of prion diseases,
also related aggregates, fibrils and polymers.
XX
Claim 11; Page 125-127; 188pp; English.
XX
The present sequence represents a yeast Sup35 protein. The protein
possesses the prion-like capacity to undergo a self-perpetuating
conformational alteration that changes the functional state of Sup35 in a
manner that creates a heritable change in phenotype. It is used to
construct chimeric polypeptides of the invention, which comprise at least
one SCHAG (self-coalesce into higher-order aggregates) amino acid
sequence fused in frame with a polypeptide of interest (which is other
than a marker protein, a glutathione-S-transferase or a staphylococcal
nuclear protein). The specification also describes chimeric polypeptides
that comprises an amyloidogenic domain that causes aggregation into
fibrils. The chimeric polypeptides are used to prepare polymers with

The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein

components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).

Query Match 100.0%; Score 701; DB 7; Length 685;
Best Local Similarity 100.0%; Pred. No. 4.4e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSNQGNQOQYQOYSGNQGNQOQGNRRYQGYQAYNAQAQAGGYQNYQYSGYQOQGY 60
DB 1 MSDSNQGNQOQYQOYSGNQGNQOQGNRRYQGYQAYNAQAQAGGYQNYQYSGYQOQGY 60
QY 61 QQYNPDAGYQOQYNPQGGYQOQYNPQGGYQOQGNPKFNFNNNLQGYQAGFPQ 120
DB 61 QQYNPDAGYQOQYNPQGGYQOQYNPQGGYQOQGNPKFNFNNNLQGYQAGFPQ 120
QY 121 SQG 123
DB 121 SQG 123

RESULT 4
AAB30800
ID AAB30800 standard; protein; 271 AA.
AC AAB30800;
XX
DT 02-APR-2001 (first entry)
XX
DE A modified N region of yeast Sup35 protein.
XX
KW Sup35; phenotype; SCHAG; self-coalesce; higher-order aggregate;
KW amyloidogenic domain; aggregation; fibril; phenotypic alteration;
KW gene therapy; disease resistance; plant pigmentation; prion disease.
OS Synthetic.
OS Saccharomyces cerevisiae.
XX
PN W0200075324-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015876.
XX
PR 09-JUN-1999; 99US-0138833P.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel T;
XX
XX
DR WPI; 2001-061723/07.
DR N-PSDB; AAC86685.
XX
PT New nucleic acid encoding chimeric proteins with self-assembly
PT properties, useful e.g. for diagnosis and treatment of prion diseases,
PT also related aggregates, fibrils and polymers.
XX
PS Claim 11; Page 135-136; 188pp; English.
XX
CC The present sequence represents a modified N region of Sup35 protein, in
CC the second oligopeptide repeat has been expanded twice, creating a total
CC of seven repeats. Sup35 possesses the prion-like capacity to undergo a
CC self-perpetuating conformational alteration that changes the functional
CC state of Sup35 in a manner that creates a heritable change in phenotype.
CC It is used to construct chimeric polypeptides of the invention, which
CC comprise at least one SCHAG (self-coalesces into higher-order aggregates)
CC amino acid sequence fused in frame with a polypeptide of interest (which
CC is other than a marker protein, a glutathione-S-transferase or a
CC staphylococcal nuclear protein). The specification also describes

chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used to create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant CC pigmentation and for diagnosis and treatment of prion diseases XX

Query Match 97.3%; Score 682; DB 4; Length 271;
Best Local Similarity 87.2%; Pred. No. 1.2e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 18; Gaps 1

Qy 1 MSDSNQGNQOQYQOYSONGNQOQGNRYQGYQAYNAQAQAGGYQYQYSGYQ--- 56
Db 1 MSDSNQGNQOQYQOYSONGNQOQGNRYQGYQAYNAQAQAGGYQYQYSGYQGGY 60

Qy 57 -----QGGYQQYNPDAGYQQOYNPQGGYQQYNPQGGYQQOYNPQGGYQY 102
Db 61 QQYNPQGGYQQYNPQGGYQQYNPDAGYQQOYNPQGGYQQYNPQGGYQQOYNPQGGY 120

Qy 103 NFNTNNNLQGYQAGFQPSQSG 123
Db 121 NFNTNNNLQGYQAGFQPSQSG 141

RESULT 5
AAB30799
ID AAB30799 standard; protein; 215 AA.
AC AAB30799;
XX
XX
DT 02-APR-2001 (first entry)
XX
DE A modified N region of yeast Sup35 protein.
XX
KW Sup35; phenotype; SCHAG; self-coalesce; higher-order aggregate;
KW amyloidogenic domain; aggregation; fibril; phenotypic alteration;
KW gene therapy; disease resistance; plant pigmentation; prion disease.
XX
OS Synthetic.
OS Saccharomyces cerevisiae.
XX
PN WO200075324-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015876.
XX
PR 09-JUN-1999; 99US-0138833P.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel T;
PI
XX
XX WPI; 2001-061723/07.
DR
DR N-PSDB; AAC86684.
XX
XX New nucleic acid encoding chimeric proteins with self-assembly
PT properties, useful e.g. for diagnosis and treatment of prion diseases,
PT also related aggregates, fibrils and polymers.
XX
XX Example 3; Page 133-134; 188pp; English.
XX

The present sequence represents a modified N region of a yeast Sup35 protein, in which four of the five oligopeptide repeats have been deleted. Sup35 possesses the prion-like capacity to undergo a self-perpetuating conformational alteration that changes the functional state of Sup35 in a manner that creates a heritable change in phenotype. It is used to construct chimeric polypeptides of the invention, which comprise at least one SCHAG (self-coalesces into higher-order aggregates) amino

PN WO2003104277-A2.
 XX 18-DEC-2003.
 XX 05-JUN-2003; 2003WO-JP007123.
 XX 05-JUN-2002; 2002JP-00164257.
 PR 06-JUN-2002; 2002US-0385912P.
 PR 26-DEC-2002; 2002JP-00377326.
 PR 27-DEC-2002; 2002US-0436457P.
 PR 15-MAY-2003; 2003JP-00137505.
 PR 16-MAY-2003; 2003US-0470836P.
 XX (ASAH) ASAH KASEI KK.
 PA Sugahara T, Mateuda A, Honda G, Muramatsu S, Ishizawa K;
 XX WPI; 2004-122214/12.
 XX N-PSDB; ADI26208.
 DR New signal transducer and activator of transcription 6 activation
 PT promoting purified protein, for diagnosing and treating disease
 PT associated with activation/inhibition of transcription factor e.g.
 PT diabetes and cancer.
 XX Claim 1; SEQ ID NO 174; 1368bp; English.
 PS The invention relates to a purified protein promoting signal transducer
 XX and activator of transcription 6 activation (STAT6). The protein is
 CC useful for the producing an antibody, which involves administering the
 CC protein or its epitope-bearing fragments to a non-human animal as an
 CC antigen. The nucleic acid is useful for diagnosing a disease or
 CC susceptibility to a disease related to expression or activity of the
 CC protein. A transformant expressing the protein is useful for screening
 CC compounds which inhibit or promote STAT6 activation. A transformant
 CC expressing the protein is useful for producing a pharmaceutical
 CC composition. Compositions, antibodies and antisense molecules are useful
 CC for the treating a disease associated with STAT6 activation such as
 CC allergic diseases, inflammation, autoimmune diseases, diabetes,
 CC hyperlipidaemia, infections disease and cancers. Compositions are useful
 CC for treating disease associated with STAT6 activation and/or prevention
 CC of Th1 hyperactive diseases. Compositions are also useful in rheumatoid
 CC arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma,
 CC allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage,
 CC viral hepatitis and AIDS. The protein has efficient promoting STAT6
 CC activity. The protein or nucleic acid is effectively useful for screening
 CC compounds for treating and preventing disease associated with excessive
 CC activation or inhibition of STAT6. The present sequence represents the
 CC amino acid sequence of a human protein which promotes STAT6 activation.
 XX SQ Sequence 592 AA;
 Query Match 23.8%; Score 167; DB 8; Length 592;
 Best Local Similarity 29.1%; Pred. No. 2.1e-08;
 Matches 46; Conservative 17; Mismatches 45; Indels 50; Gaps 7;
 QY 1 MSPDS-----NCGNNQNTQYTSQNGNQOQ-----NNRY-QGYQAYNAQAQA 42
 DB 1 MSPDSGYSQSGGEGQSYSTGNPGSQYQASQSYSGYGTDTSDSYQNTSGYSSYQSQ 60
 QY 43 GGYQNTQYSGYSGYQGYQOQ--YN-----PDAGYQQQYNNPQG 77
 DB 61 SGYSQSYSGYQENQKSSYQOQYNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNN 120
 QY 78 GYQYNNPQGGYQOQFNPQGGKGNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFN 115
 DB 121 GYDQH--QGSYDEQSN-----YDQHDYSQNNQSSYHS 151
 RESULT 10
 AAB30810
 ID AAB30810 standard; protein; 405 AA.
 XX

AC AAB30810;
 XX 02-APR-2001 (first entry)
 DT Amino acid sequence of a prion-like amyloidogenic protein.
 DE SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain;
 XX aggregation; fibril; phenotypic alteration; gene therapy;
 KW disease resistance; plant pigmentation; prion disease.
 KW Saccharomyces cerevisiae.
 OS WO200075324-A2.
 PN 14-DEC-2000.
 XX 09-JUN-2000; 2000WO-US015876.
 XX 09-JUN-1999; 99US-0138833P.
 XX (ARCH-) ARCH DEV CORP.
 PA Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel T;
 XX WPI; 2001-061723/07.
 DR New nucleic acid encoding chimeric proteins with self-assembly
 XX properties, useful e.g. for diagnosis and treatment of prion diseases,
 PT also related aggregates, fibrils and polymers.
 XX Claim 11; Page 150-152; 188bp; English.
 PS AAB30803-17 represent prion-like amyloidogenic proteins which have been
 CC identified from a yeast protein database. The specification describes
 CC chimeric polypeptides, which comprise at least one SCHAG (self-coalesces
 CC into higher-order aggregates) amino acid sequence fused in frame with a
 CC polypeptide of interest (which is other than a marker protein, a
 CC glutathione-S-transferase or a staphylococcal nuclear protein). The
 CC specification also describes chimeric polypeptides that comprises an
 CC amyloidogenic domain that causes aggregation into fibrils. The chimeric
 CC polypeptides are used to prepare polymers with multiple reactivities,
 CC e.g. derivatised with enzymes, or specific binding partners, and useful
 CC e.g. for performing multi-step chemical reactions. They can be used
 CC create an inducible, or stable phenotypic alteration in a cell, e.g. for
 CC gene therapy, protein production, imparting disease resistance to plants,
 CC altering plant pigmentation and for diagnosis and treatment of prion
 CC diseases
 XX SQ Sequence 405 AA;
 Query Match 23.7%; Score 166; DB 4; Length 405;
 Best Local Similarity 34.4%; Pred. No. 1.6e-08;
 Matches 55; Conservative 7; Mismatches 44; Indels 54; Gaps 9;
 QY 2 SDSNCGNNQNTQYTSQNGNQOQNNRNYQGYQAYNAQAQAPAGGYQNTQYSG----- 54
 DB 219 NNQNNNSNQGYNQSYQNGNQNS-----QGYN--NQYQGGNGYQOQOQSGGAFSSLA 271
 QY 55 -----YQGGYQYNNPDAGYQOQYNNPQG--GYQYNNPQG-----GYQOQNNPQG--- 96
 DB 272 SMAQSYLGGGGTQSN-----QQQYNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNN 323
 QY 97 -----GRGNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFNKFN 123
 DB 324 SFSALASMASSYLGNNSNSNSYGGQOQQAQNEVGRFQHNG 362
 RESULT 11
 AAB30821
 ID AAB30821 standard; protein; 405 AA.
 XX AAB30821;
 AC AAB30821;
 XX

KW	subarachnoid haemorrhage; viral hepatitis; AIDS.
XX	
OS	Homo sapiens.
XX	
PN	WO2003104277-A2.
XX	
PD	18-DEC-2003.
XX	
PF	05-JUN-2003; 2003WO-JP007123.
XX	
PR	05-JUN-2002; 2002JP-00164257.
PR	06-JUN-2002; 2002US-0385912P.
PR	26-DEC-2002; 2002JP-00377326.
PR	27-DEC-2002; 2002US-0436467P.
PR	15-MAY-2003; 2003JP-00137505.
PR	16-MAY-2003; 2003US-0470836P.
XX	
PA	(ASAH) ASAH KASEI KK.
XX	
PI	Sugahara T, Matsuda A, Honda G, Muramatsu S, Ishizawa K;
XX	
DR	WPI; 2004-122214/12.
DR	N-PSDB; ADI26206.
XX	
PT	New signal transducer and activator of transcription 6 activation
PT	promoting purified protein, for diagnosing and treating disease
PT	associated with activation/inhibition of transcription factor e.g.
PT	diabetes and cancer.
XX	
PS	Claim 1; SEQ ID NO 172; 1368pp; English.
XX	
CC	The invention relates to a purified protein promoting signal transducer
CC	and activator of transcription 6 activation (STAT6). The protein is
CC	useful for the producing an antibody, which involves administering the
CC	protein or its epitope-bearing fragments to a non-human animal as an
CC	antigen. The nucleic acid is useful for diagnosing a disease or
CC	susceptibility to a disease related to expression or activity of the
CC	protein. A transformant expressing the protein is useful for screening
CC	compounds which inhibit or promote STAT6 activation. A transformant
CC	expressing the protein is useful for producing a pharmaceutical
CC	composition. Compositions, antibodies and antisense molecules are useful
CC	for the treating a disease associated with STAT6 activation such as
CC	allergic diseases, inflammation, autoimmune diseases, diabetes,
CC	hyperlipidaemia, infectious disease and cancers. Compositions are useful
CC	for treating disease associated with STAT6 activation and/or prevention
CC	of Th1 hyperactive diseases. Compositions are also useful in rheumatoid
CC	arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma,
CC	allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage,
CC	viral hepatitis and AIDS. The protein has efficiently promoting STAT6
CC	activity. The protein or nucleic acid is effectively useful for screening
CC	compounds for treating and preventing disease associated with excessive
CC	activation or inhibition of STAT6. The present sequence represents the
CC	amino acid sequence of a human protein which promotes STAT6 activation.
XX	
SQ	Sequence 589 AA;

Query Match	23.3%;	Score 163.5;	DB 8;	Length 589;
Best Local Similarity	30.8%;	Pred. No. 4.7e-08;		
Matches	49;	Conservative	13;	Mismatches 42; Indels 55; Gaps 8;

QY	1	MSDS----	NGNNNQNYCQISONGNQOQNNRYQGYQAYNAQAQA-GGYQNTQGVSGY	55
Db	1	MSDSGSGYGGGEGQISYTYGNPQSGYG----	QASQSYGQYGTDTSSYQNTSGYSSY	56
QY	56	QQ-----GGY-----	QQYN-----	PDAGYQQQYNPQ
Db	57	QGSYSQSGYGVENQKQSSYSQFPYNNQQQNNMSSSGQGRAPSYQPDYDQGHSDQQ		116
QY	77	GGYQQTNPQGGYQQQFPQGRGNYKFNVNNNLQGYQA		115
Db	117	SGYDQH--QGSYDEQSN-----	YDQHDSDYSQNQQSYHS	148

RESULT 14	
AAE09770	ID AAE09770 standard; protein; 1145 AA.
AC	AAE09770;
XX	
DT	29-NOV-2001 (first entry)
XX	Drosophila melanogaster argonaute 2 protein.
DE	Fruit fly; gene expression; dicer; argonaute 2; RNA interference; RNAI;
KW	attenuation; gene function.
XN	
OS	Drosophila melanogaster.
XX	
FH	Key Location/Qualifiers
FT	Region 437..446
FT	/note= "Peptide identified by microsequencing"
FT	Region 456..462
FT	/note= "Peptide identified by microsequencing"
FT	Region 485..488
FT	/note= "Peptide identified by microsequencing"
FT	Region 548..558
FT	/note= "Peptide identified by microsequencing"
FT	Region 593..605
FT	/note= "Peptide identified by microsequencing"
FT	Region 740..745
FT	/note= "Peptide identified by microsequencing"
FT	Region 1112..1119
XX	/note= "Peptide identified by microsequencing"
PX	WO200168836-A2.
NN	
PD	20-SEP-2001.
XX	
PF	16-MAR-2001; 2001WO-US008435.
XX	
PR	16-MAR-2000; 2000US-0189739P.
PR	24-OCT-2000; 2000US-0243097P.
XX	(GENE-) GENETICA INC.
PA	(COLD-) COLD SPRING HARBOR LAB.
XX	
PI	Beach D, Bernatein E, Caudy A, Hammond S, Hannon G;
DR	WPI; 2001-565793/63.
XX	
PT	Attenuating gene expression in a cell using gene-targeted double stranded RNA.
XX	
PS	Claim 6; Fig 24; 135pp; English.
CC	The invention relates to methods for attenuating gene expression in a cell using gene targeted double stranded RNA. The double stranded RNA comprises a nucleotide sequence that hybridises under physiologic conditions of the cell to the DNA sequence of the target gene to be inhibited. The method utilises a cell in which dicer or argonaute activities are recombinantly expressed or otherwise ectopically activated. Activated RNA interference (RNAi) enzymes such as dicer and argonaute are specifically and potentially used for inactivating a cloned gene and proves to be a powerful tool for investigating gene function. Methods are used for attenuating target gene expression in non-embryonic cells suspended in culture or in animals. The present sequence is Drosophila melanogaster argonaute 2 protein related to the invention
XX	
SQ	Sequence 1145 AA;
Query Match	23.3%; Score 163; DB 4; Length 1145;
Best Local Similarity	34.2%; Pred. No. 1.2e-07;
Matches	52; Conservative 10; Mismatches 56; Indels 34; Gaps 7
YQ	6 CGNNQQ-----NYQY---SQNGNQCGNNRYQGYYAQAQAGGYYNQGY---52 : : :

Db 119 QGGHQGRGQDGGYQQRPPGQGGHQQGRGQEGGYQQRPPGQGGHQQGRGQEGG 178
QY 53 -----SGYQGGYQ--YNPDAGYQQ--YNPQGYQ--YNPQGYQ--YNPQGYQ--Q 91
Db 179 YQQRPSGQGGHQQGRGQEGGYQQRPPGQGGHQQGRGQEGGYQQRPSGQGGHQQ 238
QY 92 FNPQGRGNYNFNNNLQGYQAGFQPSOG 123
Db 239 QGRGQEGGYQQRPSGQGGHQQGRGQEGG 270

RESULT 15
ADB38846
ID ADB38846 standard; protein; 1145 AA.
XX AC ADB38846;
DT 04-DEC-2003 (first entry)
XX DE Drosophila argonaute 2 protein related to gene expression inhibitors.
XX KW attenuating expression; double stranded RNA; dsRNA; RNA interference;
KW post-transcriptional gene silencing; quelling; short inhibitory RNA;
KW siRNA; short hairpin RNA; shRNA; gene expression; gene-targeted dsRNA;
KW adult stem cell; Major Histocompatibility Complex; MHC;
KW cellular medicament; Dicer; RNAi enzyme.
XX OS Drosophila sp.
XX PN WO2003062394-A2.
XX PD 31-JUL-2003.
XX PF 22-JAN-2003; 2003WO-US001963.
XX PP 22-JAN-2002; 2002US-00055797.
XX PR (GENE-) GENETICA INC.
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PI Beach DH, Bernstein E, Caudy A, Hammond S, Hannon GJ;
XX PI Paddison PJ, Conklin D;
XX DR WPI; 2003-636734/60.

XX PT Attenuating expression of a target gene in host cells comprises
XX PT introducing double stranded RNA into the host cells in an amount that
XX PT attenuates expression of the target gene.
XX PS Disclosure: Fig 24; 150pp; English.
XX CC This invention relates to a novel method of attenuating expression of a
XX CC target gene in host cells which comprises introducing double stranded RNA
XX CC (dsRNA) into the host cells in an amount sufficient to attenuate
XX CC expression of the target gene, where the dsRNA comprises a nucleotide
XX CC sequence that hybridises under stringent conditions to an untranslated or
XX CC intronic sequence of the target gene. The method may be known as RNA
XX CC interference, post-transcriptional gene silencing or quelling and makes
XX CC use of short inhibitory RNA (siRNA) or short hairpin RNA (shRNA)
XX CC sequences. The method may be useful for attenuating gene expression in a
XX CC cell using gene-targeted dsRNA. In a preferred embodiment of the
XX CC invention, the method is used on undifferentiated adult stem cells to
XX CC increase or decrease Major Histocompatibility Complex (MHC) expression.
XX CC The stem cell is useful in manufacturing a cellular medicament for
XX CC transplantation to a patient. The composition may be used in
XX CC manufacturing a medicament for attenuating expression of one or more
XX CC genes in vivo. The present sequence is that of the Drosophila Argonaute 2
XX CC protein which is related to the invention and a homologue of the human
XX CC Dicer protein. Dicer, an RNAi enzyme, is required for shRNA mediated gene
XX CC silencing.
XX SQ Sequence 1145 AA;

Query Match 23.3%; Score 163; DB 7; Length 1145;
Best Local Similarity 34.2%; Pred. No. 1.2e-07;
Matches 52; Conservative 10; Mismatches 56; Indels 34; Gaps 7;
QY 6 QGNNQQ-----NYQY---SQNGNQGGNNRYQGYQAYNAQAQAGGYQNTYQY--- 52
Db 119 QGGHQGRGQDGGYQQRPPGQGGHQQGRGQEGGYQQRPPGQGGHQQGRGQEGG 178
QY 53 -----SGYQGGYQ--YNPDAGYQQ--YNPQGYQ--YNPQGYQ--YNPQGYQ--Q 91
Db 179 YQQRPSGQGGHQQGRGQEGGYQQRPPGQGGHQQGRGQEGGYQQRPSGQGGHQQ 238
QY 92 FNPQGRGNYNFNNNLQGYQAGFQPSOG 123
Db 239 QGRGQEGGYQQRPSGQGGHQQGRGQEGG 270

Search completed: July 1, 2005, 18:17:01
Job time : 37.3148 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 18:06:15 ; Search time 7.18756 Seconds
(without alignments)
1646.548 Million cell updates/sec

Title: US-09-591-632-2_COPY_1_123

Perfect score: 701

Sequence: 1 MSDSNQGNQYQYQSQNG.....FVYNNLQYQAGFPQSQG 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-79:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	701	100.0	685	1	EFBS2
2	166	23.7	405	2	suppressor 2 prote
3	166	23.7	741	2	hypothetical prote
4	163.5	23.3	589	2	suppressor 2 prote
5	149	21.3	456	2	RNA/esDNA-binding
6	148	21.1	419	2	protein F57B9.9 [i
7	147.5	21.0	409	2	DAG protein homolo
8	147.5	21.0	940	2	hypothetical prote
9	147.5	21.0	945	2	protein F39D8.1b [
10	147	21.0	462	1	hypothetical prote
11	144	20.5	232	2	annexin VII - slim
12	143	20.4	372	2	hypothetical prote
13	142	20.3	676	2	bifunctional endo-
14	141	20.1	404	2	hypothetical prote
15	141	20.1	800	2	synovial sarcoma t
16	140.5	20.0	236	2	dsRNA-binding prot
17	139	19.8	632	2	hypothetical trans
18	138	19.7	1111	2	hypothetical prote
19	137.5	19.6	284	2	hypothetical prote
20	137.5	19.6	765	2	hypothetical prote
21	137	19.5	455	2	hypothetical prote
22	136.5	19.5	461	2	arabingalactan-pr
23	136	19.4	462	4	FUS/CHOP mutant fu
24	136	19.4	526	1	RNA-binding protei
25	135	19.3	128	2	probable membrane
26	135	19.3	528	2	fus-like protein -
27	135	19.3	867	2	hypothetical prote
28	135	19.3	871	2	hypothetical prote
29	133	19.0	3498	2	hypothetical prote

30	132	18.8	882	2	H70199	translation initia
31	131	18.7	1161	2	T18400	glutamate-cysteine
32	128	18.3	618	2	T19407	hypothetical prote
33	128	18.3	635	2	T19403	hypothetical prote
34	126.5	18.0	738	2	S37876	glutamine-rich pro
35	124.5	17.8	382	2	T293339	hypothetical prote
36	124.5	17.8	1196	2	S65245	translation elonga
37	123	17.5	346	2	S44874	ZC21.3 protein -C
38	121.5	17.3	353	1	S56750	single stranded D
39	121	17.3	597	2	T51889	related to clathri
40	121	17.3	954	1	S20907	endo-1,4-beta-xyla
41	120.5	17.2	989	2	T02568	hypothetical prote
42	119.5	17.0	301	2	JW0079	heterogeneous nucl
43	119.5	17.0	557	2	T19686	hypothetical prote
44	119.5	17.0	1139	2	T33275	hypothetical prote
45	118.5	16.9	129	2	T06256	dormancy-associate

ALIGNMENTS

RESULT 1

EFBS2

suppressor 2 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: G1-to-S transition protein; protein YD9395.05; protein YDR172w

C:Species: Saccharomyces cerevisiae

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: S00733; S49768; S00488; A26742; S00533; S05723

R:Wilson, P.G.; Culbertson, M.R.

J. Mol. Biol. 199, 559-573, 1988

A:Title: SUP12 suppressor protein of yeast. A fusion protein related to the EF-1 family

A:Reference number: S00733; MUID:88172503; PMID:3280807

A:Accession: S00733

A:Molecule type: DNA

A:Residues: 1-685 <WIL>

R:Kushnirov, V.V.; Ter-Avanesyan, M.D.; Telckov, M.V.; Surguchov, A.P.; Smirnov, V.N.; I

Gene 66, 45-54, 1988

A:Title: Nucleotide sequence of the SUP2(SUP35) gene of Saccharomyces cerevisiae.

A:Reference number: JT0323; MUID:88329727; PMID:3047009

A:Accession: JT0323

A:Molecule type: DNA

A:Residues: 1-685 <KUS>

A:Cross-references: EMBL:M21129; NID:G172789; PIDN:AAA35133.1; PID:G172791

R:Murphy, L.; Harris, D.E.

submitted to the EMBL Data Library, November 1994

A:Reference number: S49764

A:Accession: S49768

A:Molecule type: DNA

A:Residues: 1-685 <MUR>

A:Cross-references: EMBL:Z46727; NID:G1289283; PIDN:CAA86677.1; PID:G1289287; GSPDB:GN00

R:Kikuchi, Y.; Shimatake, H.; Kikuchi, A.

EMBO J. 7, 1175-1182, 1988

A:Title: A yeast gene required for the G1-to-S transition encodes a protein containing a

A:Reference number: S00488; MUID:88296422; PMID:2841115

A:Accession: S00488

A:Molecule type: DNA

A:Residues: 1-52, 'C', 54-685 <KIK>

A:Cross-references: GB:Y00829; EMBL:Y00829; NID:G3711; PIDN:CAA68760.1; PID:G3712

C:Genetics:

A:Gene: SGD:SUP35; SUP12; GST1; SUP2; MIPS:YDR172w

A:Cross-references: SGD:S0003579; MIPS:YDR172w

A:Map position: 4R

C:Superfamily: suppressor 2 protein; translation elongation factor Tu homology

C:Keywords: duplication; GTP binding; nucleotide binding; P-loop; phosphoprotein; tandem

F:1-123/Domain: A <DOM1>

F:42-119/Region: 10-residue repeats

F:124-253/Domain: charged <DOM2>

F:159-222/Region: glutamic acid/lysine-rich

F:254-685/Domain: C <DOM4>

F:261-409/Domain: translation elongation factor Tu homology <ETU>

F:267-274/Region: nucleotide-binding motif A (P-loop)

F:406-409/Region: GTP-binding NKXD motif

RESULT 7

T20847
hypothetical protein F13E9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20847
R;McMurray, A.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19332
A;Accession: T20847
A>Status: preliminary; translated from GB/EMBL/DDBBJ
A:Molecule type: DNA
A:Residues: 1-409 <WIL>
A;Cross-references: UNIPROT:Q19414; EMBL:Z69383; PIDN:CAA93412.1; GSPDB:GN00022; CESP:F13E9
A;Experimental source: clone F13E9
C;Genetics:
A;Gene: CESP:F13E9.4
A;Map position: 4
A;Introns: 32/1; 275/3; 337/3
C;Superfamily: loricrin

Query Match 21.0%; Score 147.5; DB 2; Length 409;
Best Local Similarity 31.2%; Pred.No. 1.le-05;
Matches 48; Conservative 15; Mismatches 46; Indels 45; Gaps 8;

QY 4 SNOGNNQQYTQQ-QYSQNGNQCGNNRYQGYYAQAYNAQAAPAGGYQN-----YQGSYG YQ 56
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 55 TGQGLLESSVQQGGYQNGSQMSMGYSQ----QGIGNSQQDYGISQSOGSGMWGVQYGGSS 110
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 57 QGGYQQYNPDAGYQQYQYNPGGYQ-----QYNPQGGYQQQFNPQGGRGNYK 102
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 111 QS YGQQ-----AF AQQRPPQQGFOSNFSCQAASGMNSFGGQGGYQNGQNGFGGQSGFS 165
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 103 -----NFVNNNNLQGYQAGFPQSOGS 123
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 166 GQSWGSGNSLSANSNGNN--QGSSSYGYQ-MNQG 197

RESULT 8

D89723
protein F39D8.lb [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89723
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A;Reference number: A75000; PMID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C.ele
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; anc
A;Accession: D89723
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-940 <STO>
A;Cross-references: UNIPROT:Q814J3; GB:chr_X; PIDN:CAA93661.1; PID:g3876953; GSPDB:GN000
C;Genetics:
A;Gene: F39D8.lb
A;Map position: X

Query Match 21.0%; Score 147.5; DB 2; Length 940;
Best Local Similarity 34.9%; Pred.No. 2.7e-05;
Matches 52; Conservative 7; Mismatches 63; Indels 27; Gaps 8;

QY 1 MSDSNGNNQQNTQQYSQNGNQCGNNRYQGYYAQAYNA-AQAQ---PAGGYQNY-QGYSGY 55
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 222 VGDQNQVFDPNQGYQNGNQNTGGITGDSQSONQCYPDPNQGYQNGQYQNGQNGQNI 281
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 56 QQGYYQQYNPDAGYQQYQYNPQG--GYQQYNP-----QGYYQQOFN-----POGGRGNY 101
 | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 282 NAGGYVDNQFOGDQDNINAGGYVGNNQNGPFQDGQNGQNNYQGYQGSTLPASGEVDY 341

Db 137 QMTPYQNGYMQQQQYNTP-SQSSWPMYNGYQSQSQSQSQSSMG 185

RESULT 12

I64223

bifunctional endo-1,4-beta-xylanase homolog - Mycoplasma genitalium

C/Species: Mycoplasma genitalium

C/Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

C/Accession: I64223

R/Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Fuhrmann, J.; Nguyen, D.; Uutterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

C.A.; Venter, J.C

Science 270, 397-403, 1995

A/Title: The minimal gene complement of Mycoplasma genitalium.

A/Reference number: A64200; MUID:96026346; PMID:7569993

A/Accession: I64223

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-372 <TIGR>

A/Cross-references: UNIPROT:P47459; GB:U39699; GB:I43967; NID:g1045903; PID:g1045904; TIGR

A/Experimental source: strain G-37

C/Genetics:

A/Genetic code: SGC3

Query Match	20.4%	Score 143;	DB 2;	Length 372;
Best Local Similarity	32.7%	Pred. No. 2.5e-05;		
Matches	51;	Conservative 12;	Mismatches 55;	Indels 38; Gaps 8;

Qy	3	DSNCGNNQNNYQOYSONG-----NQOQGN-----RVQGYQAYNAQAQAGGYQYNNYQGYSG	54
Db	22	DQNOYYQDPNQOQFNQSGFDPNQOQFNQGFDPNQOYQDPNQOQFNQAGFDQNNQYYQD	81
Qy	55	-----YQGGYQYQYNDAGY-QQYNNPQGGYQOYNNPQGGYQQQF--NP	94
Db	82	PNQOQFNQGFDPNQOYQDPNQOQFN-QAGFDNQYYQDPNQOQFNQSGFDQNNQYYQDP	140
Qy	95	QGGRGNTKNNFNNNNLQYQAGFO-----PQSQ	122
Db	141	NQOQFNQPSFDLNNQ-QFNQOQFNQSGPAFETTPQEQ	175

RESULT 13
S41022 hypothetical protein T07C4.9 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41022
R:Berks, M.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41014
A:Accession: S41022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-676 <BER>
A:Cross-references: UNIPROT:Q27512; EMBL:Z29443; NID:g1067051; PID:g443836
C:Genetics:
A:Introns: 69/3; 161/1; 208/3; 227/1; 357/1; 505/3
F:373-444/Domain: annexin repeat homology <AX1>
F:445-516/Domain: annexin repeat homology <AX6>
F:528-600/Domain: annexin repeat homology <AX3>
F:604-675/Domain: annexin repeat homology <AX4>

Query Match	20.3%	Score 142;	DB 2;	Length 676;
Best Local Similarity	36.6%;	Pred. No. 5.7e-05;		
Matches	48;	Conservative 2;	Mismatches 49;	Indels 32; Gaps 7;
Qy	8	NNQNYQQYSNGNQ-QGNNRYCGYQAYNAQAQAGGYQNY-----QGVSQYQ-QGG	59	
Db	230	NQQPSYGGYGGPQQQPGYVGNSSYDPYQGPQQQPYPGGGGGPPYPGSNNGQGGYPGGG	289	
Qy	60	YQQNPDPAGYQQ--QYN-----PQGGY-----QQYNPQGGYQQQFNPQGGRGNYK	102	

Db 290 APYEGSGGYPQAPQYGFSGGSAQPQNQGGYPPQQQYPPQGGYVQGGGQOQGGGGFPF 349

QY 103 NFNTNNLQGY 113

Dd 350 N-----QGY 353

RESULT 14

S46269
synovial sarcoma translocation protein - human
N:Alternate names: SYT protein
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision
C:Date: 21-Jul-1995 #text_change 08-Oct-1999
C:Accession: S46269; S51172
R:Clark, J.; Rocques, P.J.; Crew, A.J.; Gill, S.; Shipley, J.; Chan, A.M.L.; Gusterson, N.
Nature Genet. 7, 502-508, 1994
A:Title: Identification of novel genes, SYT and SSX, involved in the t(X;18) (p11.2;q11.2) translocation
A:Reference number: S46269; MUID:95038836; PMID:7951320
A:Accession: S46269
A:Molecule type: mRNA
A:Residues: 1-404 <CLA>
A:Cross-references: EMBL:X79201
A:Note: it is uncertain whether translation is initiated upstream to the sequenced region
R:Cooper, C.S.
submitted to the EMBL Data Library, May 1994

A:Submitted to the EMBL Data Library, May 1994
 A:Reference number: S51172
 A:Accession: S51172
 A:Molecule type: mRNA
 A:Residues: 'M', 15-404 <COO>
 A:Cross-references: EMBL:X79201; NID:G531105; PIDN:CAA55792.1; PID:G531106
 C:Genetics:
 A:Gene: GDB:SSXT; SYT
 A:Cross-references: GDB:434322; OMIM:600192
 A:Map position: 18q11.2-18q11.2

Query Match	20.1%	Score 141;	DB 2;	Length 404;
Best Local Similarity	35.7%	Pred. No. 4.1e-05;		
Matches	50;	Conservative	9;	Mismatches 55;
				Indels 26;
				Gaps 10;

Qy	1	MSDSNQGNQNYQYQY-----SQNGNOO--GNRYQGYQ-AYNAQAQAPAG---GYQNY	49
Db	252	MGVNGNHHMGRQI PPRPPOQGPPQYSCQEDYGDYSHGGQGPPEGMNQYYPDG	311
Qy	50	QGYSGYQGGYQYQYNPDAGY---QQYNPQGGYQYNPQGGYQQQFNP--QGRG-NYKNF	104
Db	312	NSQYQQQDAYGPPPPQYPPQQYQGGQYP-----GQQGYGSGQGGPGQYPNY	365
Qy	105	NYNNNLQGYQ-AGFPQSQG	123
Db	366	PQG---QGCOYGGYRPTOPG	382

RESULT 15

rs3001 13
 I51653
 dsRNA-binding protein 4F.2 - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I51653
 R:Baas, B.L.; Hurst, S.R.; Singer, J.D.
 Curr. Biol. 4, 301-314, 1994
 A:Title: Binding properties of newly identified Xenopus proteins containing dsRNA-binding
 A:Reference number: I51652; MUID:95006649; PMID:7922339
 A:Accession: I51653
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-800 <BAS>
 A:Cross-references: UNIPROT:Q91551; EMBL:U07156; NID:9463904; PIDN:AAA19961.1; PID:G51434
 F:303-371/Domain: double-stranded RNA-binding repeat homology <DSR1>

Query Match	20.1%;	Score 141;	DB 2;	Length 800;
Best Local Similarity	31.3%;	Pred. No. 8.2e-05;		
Matches 46;	Conservative	9;	Mismatches 46;	Indels 46;
				Gaps 9

QY 7 GNNQO-----NYQQYSQNGNQO-----QGNNRYQGY---QAYNA----- 37
 Db 573 GNNYQTSATAGYSQFYNSGCGASGAGGAGSGYSSYQEGYNAPTPPKFVKKPPPP 632
 QY 38 --QAQAGGYYQN-----YQYSGYQGGYQQYNPDAGYQQQYNPQGGYQQYNP-----Q 85
 Db 633 QQQQQPPPHASNPKPSPSYNGYQGH-QGGQQQQPQQQQQQTYN-QNYSNYGPQKQK 690
 QY 86 GGYQQQFNPQGGRGYNKFNNNNQQ 112
 Db 691 GGYNQGTQGAASAGSY---NYSNYSYG 714

Search completed: July 1, 2005, 18:21:01
Job time : 10.1876 secs

RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SCI15;
RX	MEDLINE=22773310; PubMed=12890024;
RA	Resende C.G., Outeiro T.F., Sands L., Lindquist S., Tuite M.P.;
RT	"Prion protein gene polymorphisms in Saccharomyces cerevisiae.";
RL	Mol. Microbiol. 49:1005-1017(2003).
DR	EMBL; AY028658; AAK26189.1; -.
KW	Prion.
FT	NON TER 233 233
FW	NON TER 233 AA; 26377 MW; 2A33D00ED1B3625D CRC64;
SQ	SEQUENCE 233 AA; 26377 MW; 2A33D00ED1B3625D CRC64;
Query Match	99.4%; Score 697; DB 2; Length 233;
Best Local Similarity	99.2%; Pred. No. 6.2e-50;
Matches 122; Conservative	0; Mismatches 1; Indels 0; Gaps 0
Qy	1 MSDSNQGNNQNYQQYSSNGNQOQGNRRYQGYQAYNAQAQPAGGYQNYQGYSGYQCGGY 60
Dd	1 MSDSNQGNNQNYQQYSSNGNQOQGNRRYQGYQAYNAQAQPAGGYQNYQGYSGYQCGGY 60
Qy	61 QQYNPDAGYQQQYNPQGGYQQQYNPQGGYQQQFNPGGGRGNTKFNFNNNNLQGYAQGFQ 120
Dd	61 QQYNPDAGYQQQYNPQGGYQQQYNPQGGYQQQFNPGGGRGNTKFNFNNNNLQGYAQGFQ 120
Qy	121 SQG 123
Dd	121 SQG 123
RESULT 10	
Q8TFR1	ID Q8TFR1 PRELIMINARY; PRT; 235 AA.
AC	Q8TFR1;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Prion protein (Fragment).
GN	Name=SUP35;
OS	Saccharomyces cerevisiae (Baker's yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX	NCBI_taxid=4932;
[1]	
RN	SEQUENCE FROM N.A.
RC	STRAIN=SCI12;
RX	MEDLINE=22773310; PubMed=12890024;
RA	Resende C.G., Outeiro T.F., Sands L., Lindquist S., Tuite M.P.;
RT	"Prion protein gene polymorphisms in Saccharomyces cerevisiae.";
RL	Mol. Microbiol. 49:1005-1017(2003).
DR	EMBL; AY028655; AAK26186.1; -.
KW	Prion.
FT	NON TER 235 235
FW	NON TER 235 AA; 26506 MW; 3E22AA89DA5A8C1D CRC64;
SQ	SEQUENCE 235 AA; 26506 MW; 3E22AA89DA5A8C1D CRC64;
Query Match	99.3%; Score 696; DB 2; Length 235;
Best Local Similarity	99.2%; Pred. No. 7.5e-50;
Matches 122; Conservative	1; Mismatches 0; Indels 0; Gaps 0
Qy	1 MSDSNQGNNQNYQQYSSNGNQOQGNRRYQGYQAYNAQAQPAGGYQNYQGYSGYQCGGY 60
Dd	1 MSDSNQGNNQNYQQYSSNGNQOQGNRRYQGYQAYNAQAQPAGGYQNYQGYSGYQCGGY 60
Qy	61 QQYNPDAGYQQQYNPQGGYQQQYNPQGGYQQQFNPGGGRGNTKFNFNNNNLQGYAQGFQ 120
Dd	61 QQYNPDAGYQQQYNPQGGYQQQYNPQGGYQQQFNPGGGRGNTKFNFNNNNLQGYAQGFQ 120
Qy	121 SQG 123
Dd	121 SQG 123
RESULT 11	
Q8TFR3	

```
Db 1 MSDSNGNNQNYQYTSQNGNQOQGNRRYQGYAYNAQAQAGGYQNYQYSGYQGGY 60
QY 61 QYNPDAGYQQQYNPQGGYQQYNPQGGYQQQYAYNAQAQAGGYQNYQYSGYQGGY 120
Db 61 QYNPDAGYQQQYNPQGGYQQYNPQGGYQQQYAYNAQAQAGGYQNYQYSGYQGGY 120
QY 121 SQ 122
Db 121 SQ 122

RESULT 13
Q96TL8 PRELIMINARY; PRT; 251 AA.
AC Q96TL8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Sup35p (Fragment).
GN Name=Sup35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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RC STRAIN=YJM273, YJM434, and YJM454;
RX MEDLINE=21518585; PubMed=11606530;
RA Jensen M.A., True H.L., Chernoff Y.O., Lindquist S.;
RT "Molecular population genetics and evolution of a prion-like protein
in Saccharomyces cerevisiae.";
RL Genetics 159:527-535(2001).
DR EMBL; AY052605; AAL15020.1; -
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
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RC STRAIN=W303, 74D694, S288C, YJM145, and YJM210;
RX MEDLINE=21518585; PubMed=11606530;
RA Jensen M.A., True H.L., Chernoff Y.O., Lindquist S.;
RT "Molecular population genetics and evolution of a prion-like protein
in Saccharomyces cerevisiae.";
RL Genetics 159:527-535(2001).
DR EMBL; AY052605; AAL15020.1; -
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OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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OX NCBI_TaxID=4932;
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RX MEDLINE=21518585; PubMed=11606530;
RA Jensen M.A., True H.L., Chernoff Y.O., Lindquist S.;
RT "Molecular population genetics and evolution of a prion-like protein
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DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Sup35p (Fragment).
GN Name=Sup35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YJM311;
RX MEDLINE=21518585; PubMed=11606530;
RA Jensen M.A., True H.L., Chernoff Y.O., Lindquist S.;
RT "Molecular population genetics and evolution of a prion-like protein
in Saccharomyces cerevisiae.";
RL Genetics 159:527-535(2001).
DR EMBL; AY052606; AAL15021.1; -
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 28372 MW; D56F94D4811C3A8A CRC64;

Query Match 98.7%; Score 692; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
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QY 3 DSNQGNQNYQYTSQNGNQOQGNRRYQGYAYNAQAQAGGYQNYQYSGYQGGYQQ 62
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Db 121 G 121
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Search completed: July 1, 2005, 18:19:52
Job time : 20.5919 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2005, 18:17:24 ; Search time 9.04241 Seconds
(without alignments)
· 1015.419 Million cell updates

Title: US-09-591-632-2 COPY 1 123

Perfect score: 701
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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 s

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

COMPARISONS

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3	141	20.1	392	4	US-09-949-016-10150	Sequence 10150, A	
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5	136	19.4	526	4	US-09-538-092-1080	Sequence 1080, Ap	
6	129	18.4	253	4	US-09-248-796A-19227	Sequence 19227, A	
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ALIGNMENTS

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; Sequence 70, Application US/10029180
; Patent No. 6806082
; GENERAL INFORMATION:
; APPLICANT: Cali, Brian M.
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin T.
; APPLICANT: Milna, G. Todd
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeffrey C.
; APPLICANT: Trueheart, Josh
; APPLICANT: Zhang, Lixin
; TITLE OF INVENTION: No. 6806082el Regulators of Fungal Gene Expression
; FILE REFERENCE: MIC-004
; CURRENT APPLICATION NUMBER: US/10/029,180
; CURRENT FILING DATE: 2001-12-22
; PRIOR APPLICATION NUMBER: US 60/257,431
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fungal gene
; US-10-029-180-70

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; Sequence 6646, Application US/09949016
; Patent No. 6812339


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; FILING DATE: 13-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Feiber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-390-200-2

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

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SUMMARIES

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10	163	23.3	1145	14	Sequence 5, Appli
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36	127	18.1	477	16	US-10-425-115-211329	Sequence 211329, A
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40	125	17.8	631	15	US-10-424-599-266585	Sequence 266585, A
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42	123.5	17.6	404	16	US-10-723-860-2047	Sequence 2047, Ap
43	122	17.4	156	16	US-10-767-701-32073	Sequence 32073, A
44	121.5	17.3	349	15	US-10-425-114-41487	Sequence 41487, A
45	121.5	17.3	1586	15	US-10-282-122A-49391	Sequence 49391, A

ALIGNMENTS

RESULT 1
US-10-732-923-17486
; Sequence 17486, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17486
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Candida maltosa
US-10-732-923-17486

Query Match 32.7%; Score 229.5; DB 17; Length 712;
Best Local Similarity 48.8%; Pred. No. 1.6e-14;
Matches 60; Conservative 7; Mismatches 43; Indels 13; Gaps 7;

Qy	4	SNQNNQNYQYQSQ-NGNQOQGNRRYQGYQAYNAQAQPA-GGYYQNYQSGYQOQGYQ 61
Db	22	SKPQQQQPQQQQYFNPNAQAQFVPTGGYQOFPQOQQQYGGYQON---YTOYQAGGYQ 78
Qy	62	Q-YNPDAGYQQQYNPQGGYQ-QYNPQGGYQQQFNPQGGRGNYKNPNYNNNQGYYQAGFQ 119
Db	79	QYNNRRGGYQQYNNRRGGYQQYNNRRGGYQQOQQQQQ-----YQAYNPQOYGGYQA-YNP 132
Qy	120	QSQ 122
Db	133	QQQ 135

```
RESULT 2
US-10-032-585-7274
; Sequence 7274, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7274
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7274

Query Match      31.8%; Score 223; DB 14; Length 721;
Best Local Similarity 43.4%; Pred. No. 7.2e-14;
Matches 59; Conservative 11; Mismatches 42; Indels 24; Gaps 9;

QY      8 NNQNNYQQY-----SONGN-----QQGNNRYQGYQAYNAQAQ-----PAGGY--YQNYQ 50
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 SDQNTQDQLSCAMANASLNGPSKQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 61

QY      51 GYSGYQQ--GGYQQNP-DAGYQQNP-PGGYQQ--YNPQGGYQQQPNPQGGRGNNKNNFN 107
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 PQQQQQQQGGYQNYQYQGGYQQYNNRGGYQQGNNRGGYQQYNNRGGYQQYNNRGGYQQYNNR 118

QY      108 NNLCGYQA-GFQPSQ 122
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      119 QQYGGYQQNSQPQQ 134

RESULT 3
US-10-732-923-17479
; Sequence 17479, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17479
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Debaryomyces hansenii
US-10-732-923-17479

Query Match      27.7%; Score 194.5; DB 17; Length 701;
Best Local Similarity 38.5%; Pred. No. 5e-11;
Matches 60; Conservative 8; Mismatches 31; Indels 57; Gaps 12;

QY      1 MSDSNQGN-----NQNNYQQYSONGNQQQQQQQQNNRYQGYQAYNAQAQA 42
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MSDDQQYNQDKLQDFQNTSIGSGEQQQQSYQYQQ-----QPOQNN-----FNANSAPT 50

QY      43 -----GGYQNYQ--GYSGYQQGYQQYNNPDAGYQQQYNNPQGGYQQY--NPQGGY 88
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      51 FTSGQQGGYQGGYQGGYQGGYQNNYNNRGGYQNNY--QGY-QYNYQ--GYQGYQNNRGGY 105

QY      89 QQQFNPQGGRGNNKNNFNNNNLLQYQAGFQP-QSQG 123
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 106 -NSYNNRGYNNYNNYNN-----QQDQQPQVQNG 132

RESULT 4

```
US-10-732-923-17478
; Sequence 17478, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17478
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Zygosaccharomyces rouxii
US-10-732-923-17478
```

```
Query Match      27.1%; Score 190; DB 17; Length 662;
Best Local Similarity 46.8%; Pred. No. 1.3e-10;
Matches 58; Conservative 1; Mismatches 39; Indels 26; Gaps 10;

QY      1 MSDSNQGNQQYQQYSONGNQQGNNRYQGY-QAYNAQAQAGGYQYNNYQGYSGYQQGG 59
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MSDPNQ-NGQ-----QGGQQNAGNNYQQYFQKLTQQAQ-AGGYQPYGGYGGY--GG 49

QY      60 YQYNNPDAGYQQYNNPQGGYQ-QYNNPQGGYQQQFNPQGGRGNNKNNFNNNN-OGYQAGFQ 118
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      50 YGYQYGGYQQPY--QDQQQAQQGAYNGPYQ--AQQAPGGFN--NYNNQ-----FQ 96

QY      119 PQSQ 122
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      97 PQQQ 100
```

RESULT 5

```
US-10-732-923-17477
; Sequence 17477, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17477
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Yarrowia lipolytica
US-10-732-923-17477
```

```
Query Match      25.0%; Score 175; DB 17; Length 742;
Best Local Similarity 35.1%; Pred. No. 4.9e-09;
Matches 59; Conservative 7; Mismatches 44; Indels 58; Gaps 11;

QY      1 MSDS-NQGN-NQNNYQQYVQ-NGNQQQGNNRYQGYQAYNAQAQ----- 40
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MSDFNQDQFANKANINSGGQGGQGGQGG-----QGYQYQAPQPFVPGQSFPVPGQ 56

QY      41 ---PAGGYQNYQYSGYQ-----QGYQYQYNNP-----DAGYQYQYNNP 75
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      57 SFAQGGYDQ-YQGGYQGGYQGGYQGGYQGGYQGGYQGGYQGGYQGGYQGGYQGGY 115

QY      76 QGGYQYNNPQGGYQQQFNPQGG-RGNNKNNFNNNNLLQYQAGFQPSQ 122
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      116 QGGYQY-QYQGGYDNYGNGQGYQGGY-----DNQYGYDQPEPQEK 156
```



```

RESULT 8
US-09-866-557A-5
; Sequence 5, Application US/09866557A
; Patent No. US20020162126A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, S.
; APPLICANT: Hannon, G.
; APPLICANT: Beach, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
; FILE REFERENCE: GNCA-P02-007
; CURRENT APPLICATION NUMBER: US/09/866,557A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/189,739
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/243,097
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-866-557A-5

Query Match      23.3%; Score 163; DB 9; Length 1145;
Best Local Similarity 34.2%; Pred. No. 1.3e-07;
Matches 52; Conservative 10; Mismatches 56; Indels 34; Gaps 7;

Qy      6  QGNNOQ-----NYQY---SSNGNQOQGNRRYQGYQAYNAQAQAPAGGYQNYQGY--- 52
Db      119 QGHQOQROGQDGGYQRPFGQGGHQQGRQGGEGYQRPFGQGGHQQGRQGGEGG 178
Qy      53  -----SCYQGGYQO---YNPDAGYQOQ---YNPQGGYQO---YNPQGGYQO-----Q 91
Db      179 YQRPSPQQQGGHQQGRQGGEGYQRPFGQGGHQQGRQGGEGYQRPSPQQQGGHQQ 238
Qy      92  FNPQGGRGNGKFNFNNNLNQYQAGFQPSQG 123
Db      239 QGRQGGEGYQRPSPGQGGHQQGRQGGEGG 270

RESULT 9
US-09-858-862-5
; Sequence 5, Application US/09858862
; Publication No. US20040018999A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, S.
; APPLICANT: Hannon, G.
; APPLICANT: Beach, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
; FILE REFERENCE: GNCA-P01-007
; CURRENT APPLICATION NUMBER: US/09/858,862
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/US01/08435
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/243,097
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/189,739
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-858-862-5

Query Match      23.3%; Score 163; DB 11; Length 1145;
Best Local Similarity 34.2%; Pred. No. 1.3e-07;
Matches 52; Conservative 10; Mismatches 56; Indels 34; Gaps 7;

Qy      6  QGNNOQ-----NYQY---SSNGNQOQGNRRYQGYQAYNAQAQAPAGGYQNYQGY--- 52

```

```
Db 119 QGHHQGRQDGGYQORPPGQGGHQQGRQGGYQORPPGQGGHQQGRQGG 178
QY 53 -----SGYQGGYQO--YNPDAGYQOQ--YNPQGGYQO--YNPQGGYQO-----Q 91
Db 179 YQORPPSGQQGGHQQGRQGGYQORPPGQGGHQQGRQGGYQORPPSGQQGGHQQ 238
QY 92 FNPQGGRGNYKNFNNNNNLQGYQAGFPQSQG 123
Db 239 QGRQGGEGGYQORPPSGQQGGHQQGRQGGEGG 270

RESULT 10
US-10-055-797-5
; Sequence 5, Application US/10055797
; Publication No. US20030084471A1
; GENERAL INFORMATION:
; APPLICANT: Hammond et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
; FILE REFERENCE: GNCA-P03-007
; CURRENT APPLICATION NUMBER: US/10/055,797
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/189,739
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-055-797-5
```

```
Query Match 23.3%; Score 163; DB 14; Length 1145;
Best Local Similarity 34.2%; Pred. No. 1.3e-07;
Matches 52; Conservative 10; Mismatches 56; Indels 34; Gaps 7;

QY 6 QGNNQO-----NYQOY---SONGNQOQGNRRYQGYQAYNAQAQAPAGGYQNYQY--- 52
Db 119 QGHHQGRQDGGYQORPPGQGGHQQGRQGGYQORPPGQGGHQQGRQGGEGG 178
QY 53 -----SGYQGGYQO--YNPDAGYQOQ--YNPQGGYQO--YNPQGGYQO-----Q 91
Db 179 YQORPPSGQQGGHQQGRQGGYQORPPGQGGHQQGRQGGYQORPPSGQQGGHQQ 238
QY 92 FNPQGGRGNYKNFNNNNNLQGYQAGFPQSQG 123
Db 239 QGRQGGEGGYQORPPSGQQGGHQQGRQGGEGG 270
```

```
RESULT 11
US-10-350-798-5
; Sequence 5, Application US/10350798
; Publication No. US2004008684A1
; GENERAL INFORMATION:
; APPLICANT: Hammond et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
; FILE REFERENCE: CSHL-P04-010
; CURRENT APPLICATION NUMBER: US/10/350,798
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/189,739
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 09/866,557
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/858,862
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/US01/08435
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/243,097
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/189,739
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.2
```

```
; SEQ ID NO 5
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-350-798-5

Query Match 23.3%; Score 163; DB 15; Length 1145;
Best Local Similarity 34.2%; Pred. No. 1.3e-07;
Matches 52; Conservative 10; Mismatches 56; Indels 34; Gaps 7;
```

```
QY 6 QGNNQO-----NYQOY---SONGNQOQGNRRYQGYQAYNAQAQAPAGGYQNYQY--- 52
Db 119 QGHHQGRQDGGYQORPPGQGGHQQGRQGGYQORPPGQGGHQQGRQGGEGG 178
QY 53 -----SGYQGGYQO--YNPDAGYQOQ--YNPQGGYQO--YNPQGGYQO-----Q 91
Db 179 YQORPPSGQQGGHQQGRQGGYQORPPGQGGHQQGRQGGYQORPPSGQQGGHQQ 238
QY 92 FNPQGGRGNYKNFNNNNNLQGYQAGFPQSQG 123
Db 239 QGRQGGEGGYQORPPSGQQGGHQQGRQGGEGG 270
```

```
RESULT 12
US-10-437-963-109378
; Sequence 109378, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109378
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13541C.1.pap
US-10-437-963-109378
```

```
Query Match 21.9%; Score 153.5; DB 16; Length 671;
Best Local Similarity 34.4%; Pred. No. 6.3e-07;
Matches 42; Conservative 9; Mismatches 50; Indels 21; Gaps 5;

QY 6 QGNNQOQYQYSQNGNQOQGNRRYQGYQAYNAQAQAPAGGYQNYQYSGY-QQGGYQOYN 64
Db 550 RGMGRGGYGGYGGYGNNGGYNQ-----GGGYDNGGGYGGYDNGGGYGGYD 596
QY 65 PDAGY---QQYNPQGGYQOQYNPQGGYQOQYNPQGGYQOQYNPQGGYQOQYAGFPQ 121
Db 597 NQGGYGGGGYGYN-QGRYGNQENGYNRGRGMRGNW---NYRGGYRGRGGGPPGG 652
QY 122 QG 123
Db 653 RG 654
```

```
RESULT 13
US-10-156-761-14380
; Sequence 14380, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
```


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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1348	100.0	685	4	AAB30792	AAB30792	Amino aci
2	1348	100.0	685	6	AAB53107	AAB53107	Protein s
3	1348	100.0	685	7	ADK63022	ADK63022	Disease t
4	1329	98.6	271	4	AAB30800	AAB30800	A modifie
5	1097	81.4	215	4	AAB30799	AAB30799	A modifie
6	485	36.0	721	5	ABP73437	ABP73437	Candida a
7	483	35.8	715	4	AAB30820	AAB30820	Amino aci
8	374.5	27.8	741	4	AAB30819	AAB30819	Amino aci
9	186	13.8	1145	4	AAB509770	AAB509770	Drosophil
10	186	13.8	1145	7	ADB38846	ADB38846	Drosophil
11	182.5	13.5	882	6	ABU19350	ABU19350	Protein e
12	175.5	13.0	407	1	ADP94879	ADP94879	ORF incor
13	169	12.5	720	7	ADB70240	ADB70240	C. neofor
14	168.5	12.5	405	4	AAB30810	AAB30810	Amino aci
15	168.5	12.5	405	4	AAB30821	AAB30821	Amino aci
16	167	12.4	592	6	ABO53050	ABO53050	Human put
17	167	12.4	592	8	ADI26209	ADI26209	Human pro
18	163.5	12.1	589	8	ADI26207	ADI26207	Human pro
19	153	11.4	952	6	ABR52717	ABR52717	Protein s
20	153	11.4	952	7	ADK61942	ADK61942	Disease t
21	151	11.2	492	7	ADJ69335	ADJ69335	Human hea
22	151	11.2	1844	3	AAB18250	AAB18250	Plasm modu
23	150.5	11.2	914	6	ABR52593	ABR52593	Protein s
24	150.5	11.2	914	7	ADK61944	ADK61944	Disease t
25	150	11.1	461	2	AAR75506	AAR75506	Nicotiana

introducing double stranded RNA into the host cells in an amount that
attenuates expression of the target gene.

Disclosure; Fig 24; 150pp; English.

This invention relates to a novel method of attenuating expression of a
target gene in host cells which comprises introducing double stranded RNA
(dsRNA) into the host cells in an amount sufficient to attenuate
expression of the target gene, where the dsRNA comprises a nucleotide
sequence that hybridises under stringent conditions to an untranslated or
intronic sequence of the target gene. The method may be known as RNA
interference, post-transcriptional gene silencing or quelling and makes
use of short inhibitory RNA (siRNA) or short hairpin RNA (shRNA)
sequences. The method may be useful for attenuating gene expression in a
cell using gene-targeted dsRNA. In a preferred embodiment of the
invention, the method is used on undifferentiated adult stem cells to
increase or decrease Major Histocompatibility Complex (MHC) expression.
The stem cell is useful in manufacturing a cellular medicament for
transplantation to a patient. The composition may be used in
manufacturing a medicament for attenuating expression of one or more
genes *in vivo*. The present sequence is that of the *Drosophila* Argonaute 2
protein which is related to the invention and a homologue of the human
Dicer protein. Dicer, an RNai enzyme, is required for shRNA mediated gene
silencing.

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA23220.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 47274; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC [ftp.wipo.int/pub/published/pct_sequences](http://www.wipo.int/pub/published/pct_sequences)

PT	introducing double stranded RNA into the host cells in an amount that
PR	attenuates expression of the target gene.
XX	Disclosure; Fig 24; 150pp; English.
CC	This invention relates to a novel method of attenuating expression of a
CC	target gene in host cells which comprises introducing double stranded RNA
CC	(dsRNA) into the host cells in an amount sufficient to attenuate
CC	expression of the target gene, where the dsRNA comprises a nucleotide
CC	sequence that hybridises under stringent conditions to an untranslated or
CC	intronic sequence of the target gene. The method may be known as RNA
CC	interference, post-transcriptional gene silencing or quelling and makes
CC	use of short inhibitory RNA (siRNA) or short hairpin RNA (shRNA)
CC	sequences. The method may be useful for attenuating gene expression in a
CC	cell using gene-targeted dsRNA. In a preferred embodiment of the
CC	invention, the method is used on undifferentiated adult stem cells to
CC	increase or decrease Major Histocompatibility Complex (MHC) expression.
CC	The stem cell is useful in manufacturing a cellular medicament for
CC	transplantation to a patient. The composition may be used in
CC	manufacturing a medicament for attenuating expression of one or more
CC	genes in vivo. The present sequence is that of the Drosophila Argonaute 2
CC	protein in which is related to the invention and a homologue of the human
CC	Dicer protein. Dicer, an RNai enzyme, is required for shRNA mediated gene
CC	silencing.
XX	
SQ	Sequence 1145 AA;
	Query Match 13.8%; Score 186; DB 7; Length 1145;
	Best Local Similarity 33.9%; Pred No. 1.9e-06;
	Matches 58; Conservative 15; Mismatches 54; Indels 44; Gaps 9
Qy	6 QGNNQ-----NYQY---SQNGNQQGNNRYGYQAYNAQAQAGGYNYQGY--- 52
Db	165 QGHQGGHQRGGEGGYQRRPSSGQQCGHQGRQGEGGYQRRPPGQCGHGQCRQGEGG 224
Qy	53 -----SGYQGGYQO--YNPDAGYQQYN--PGGYQO--YNPQGYQOO--FNPQGGRG 99
Db	225 YQRRPSSGQQCGHGQGRQGEGGYQRRPSSGQQCGHQGRQGEGGYQRRPPGQCGHGQCRQGEGG 224
Qy	100 NYKNFNYYNNLQGYQAGFPQSQGSMLNDFOK-----QQKQAAAPKP 140
Db	283 -----HQGHQGGEGGYQRRPFGQGPQNTQSQGYQSRGPPQDQAAALPLP 327
RESULT 11	
ABU19350	
ID	ABU19350 standard; protein; 882 AA.
AC	ABU19350;
XX	
DT	19-JUN-2003 (first entry)
XX	
DE	Protein encoded by Prokaryotic essential gene #4877.
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.
OS	Borrelia burgdorferi.
XX	
PN	WO200277183-A2.
PD	
XX	03-OCT-2002.
XX	
PF	21-MAR-2002; 2002WO-US009107.
XX	
PR	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	
PA	(ELIT-) ELITRA PHARM INC.
PI	Wang L, Zamudio C, Malone C, Haselebeck R, Ohlsen KL, Zyskind JW;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:17:24 ; Search time 18.5994 Seconds
(without alignments)
1015.419 Million cell updates/sec

Title: US-09-591-632-2_COPY_1_253

Perfect score: 1348

Sequence: 1 MSDSNQGNQYQYSQNG.....SADALIKQEBEVDDEVND 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269	20.0	159	4	US-09-248-796A-19824
2	230.5	17.1	139	4	US-09-248-796A-19825
3	151.5	11.2	1196	4	US-09-248-796A-19876
4	148.5	11.0	207	4	US-10-029-180-70
5	146.5	10.9	462	2	US-09-919-039-324
6	145	10.8	1162	2	US-08-728-323A-2
7	145	10.8	1162	3	US-09-298-568-2
8	145	10.8	1162	4	US-09-410-399-2
9	145	10.8	1162	4	US-09-894-273-2
10	143.5	10.6	391	4	US-09-949-016-6646
11	143.5	10.6	392	4	US-09-949-016-10150
12	142.5	10.6	1010	4	US-09-248-796A-16379
13	140.5	10.4	657	4	US-09-248-796A-19232
14	136	10.1	526	4	US-09-538-092-1080
15	135.5	10.1	545	4	US-09-248-796A-15777
16	134.5	10.0	210	4	US-09-248-796A-25835
17	134.5	10.0	588	4	US-09-248-796A-20839
18	134.5	10.0	980	4	US-09-248-796A-19242
19	134	9.9	284	4	US-09-902-540-12642
20	133	9.9	177	4	US-09-248-796A-19826
21	132.5	9.8	1020	4	US-09-538-092-911
22	131	9.7	1179	4	US-09-949-016-7088
23	129.5	9.6	907	4	US-09-949-016-9750
24	129.5	9.6	907	4	US-09-949-016-9751
25	129	9.6	253	4	US-09-248-796A-19227
26	128	9.5	455	4	US-09-248-796A-23564
27	128	9.5	555	4	US-09-248-796A-20471

28	127	9.4	180	4	US-10-029-180-38	Sequence 38, Appl
29	127	9.4	286	4	US-09-248-796A-16992	Sequence 16992, A
30	127	9.4	461	2	US-08-630-822A-68	Sequence 68, Appl
31	127	9.4	461	2	US-09-005-069-68	Sequence 68, Appl
32	127	9.4	461	3	US-09-171-156A-27	Sequence 27, Appl
33	127	9.4	461	4	US-09-004-730A-27	Sequence 27, Appl
34	127	9.4	461	4	US-08-981-799A-27	Sequence 27, Appl
35	127	9.4	494	4	US-09-248-796A-14156	Sequence 14156, A
36	127	9.4	515	4	US-09-248-796A-20270	Sequence 20270, A
37	126.5	9.4	229	4	US-09-248-796A-24831	Sequence 24831, A
38	125.5	9.3	485	2	US-08-749-391-2	Sequence 2, Appl
39	125.5	9.3	485	3	US-09-390-200-2	Sequence 2, Appl
40	125	9.3	733	3	US-08-725-459B-21	Sequence 21, Appl
41	123.5	9.2	530	4	US-09-121-211-2	Sequence 2, Appl
42	123.5	9.2	538	4	US-09-949-016-9363	Sequence 9363, Ap
43	123.5	9.2	954	4	US-09-570-856B-31	Sequence 31, Appl
44	123.5	9.2	1187	4	US-09-949-016-7933	Sequence 7933, Ap
45	122	9.1	351	4	US-09-121-211-22	Sequence 22, Appl

RESULT 1

US-09-248-796A-19824

US-09-248-796A-19824, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 19824

LENGTH: 159

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-19824

Query Match 20.0%; Score 269; DB 4; Length 159;

Best Local Similarity 42.3%; Pred. No. 5.7e-16;

Matches 74; Conservative 12; Mismatches 41; Indels 48; Gaps 8;

QY 55 YQQGGYQYNDAGYQQYNNPQGGYQQYNNPQ---GGYQQQFNPOGGRGNYKNFNNNLQ 111

DB 7 YQQG---YNNRGGYQQYNNRGGYQQYNNQYGGYQ-----YNSOPQ 47

QY 112 GYQAGFQSQGMSLNDFOKQ--QKQAA---PKPKTKLVSSSGIKLANATKKVGT--K 164

DB 48 QQQ---QQQSQGMSLADFKQTEQQASLNKPAVKTKLKLAGSSIKLANATKKVDTTYSK 104

QY 165 P-----AESDKBEKGAETKEPTKEPTKVEEPVKKEKPVOTE 203

DB 105 PQSKESPAPAPAPTASASTASQBEKBEKEAAATTPAAPETKETSAPATK 159

RESULT 2

US-09-248-796A-19825

US-09-248-796A-19825, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

```

; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19825
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19825

Query Match      17.1%; Score 230.5; DB 4; Length 139;
Best Local Similarity 40.7%; Pred. No. 1.1e-12;
Matches 66; Conservative 10; Mismatches 31; Indels 55; Gaps 7;

QY 63 YNPDAGY-QQYNPOGGYQQYNPOGGYQQQFNPQGGRGNYKNFNYNNNLOGYQAGFQPS 121
Db : |||
4 FQPAGEYQWQY---GGYQQYNSPQQQQ-----QQQS 33

QY 122 QGMSLNDPQKQ-OKQAA---PKPKTKLKVSSSGIKLANATKKVGT--KP-----165
Db : |||
34 QGMSLADPQKQKTQQQASLNKPAVKTKLKLKAGSSGIKLANATKKVDTTTSKPQKSSPAP 93

QY 166 -----AESDKVEEKSAAETKEPTKEPTKVEBPVKKEKP 199
Db :: :|||
94 APAFAAFASQBEKKEEKAATAATPETKNETSAPAETKKEPTT 135

RESULT 3
US-09-248-796A-19876
; Sequence 19876, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19876
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Candida albicans
; NAME/KEY: UNSURE
; LOCATION: (491)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-19876

Query Match      11.2%; Score 151.5; DB 4; Length 1196;
Best Local Similarity 26.5%; Pred. No. 0.00013;
Matches 62; Conservative 30; Mismatches 105; Indels 37; Gaps 10;

QY 11 QNYQQYSQNGNQOQGNRRYQGYAYNAQAPAGGYQNYQYSGYQ--QGGYQQYNPDAG 68
Db :: :|||
4 KSGDDPIKQKQKQSKPKGFGYRNNN-----QGGYNNY-QAYGNVTFPGNGQQFQYQGG 57

QY 69 YQQYNPOGGYQQYNPOGGYQQQFNPQGGRGNYKNFNYNNNLOGYQAGFQPSQGSMLN- 127
Db : |||
58 YNQGFNQ--QYQYQGGYNNQGYNSNNYNNNNNTN-----QSTISTPV 107

QY 128 DFKQKQKQAPKPKTKLKVSSSGIKLANATKKVGTKPAESDKKEEKSAAETKEPTKEPT 187
Db : |||
108 DSLPSTSGRSTPNAS--TTSLTSLNTALAKLVNSNIPFEENLSNIEKAGKTAETRPE--163

QY 188 KYEPPVKKEKPQVTEETKEKSELPKVEDLKISSTHNNNANVTSDALIKE 241
Db : :|||
164 -VETIVK-----IDQEDLSINEWKLNELKLSLK---PKSPALVKE 203

```


Matches	75; Conservative	33; Mismatches	130; Indels	75; Gaps	14;
QY	2	SDSNQGN--NQONTQY	SSQNGNQGNRYQGY	QAYNAQAQ	PAGGYQYQNYQGYSGYQO-- 57
		:	:	:	:
Db	84	SQSQSSYQOQSSYPGY	QQPAPSTSGSY	SSQSSSYQOQSSY	QOQSSYQOQSSYQOQSSY 143
		:	:	:	:
QY	58	GGYQQYNPDAGY--QQY	YNPQ-----	GGYQQYNP-----	84
		:	:	:	:
Db	144	GOQSSYNPPQGYQOQ	NYNSSGGGGGGGGG	GNYQDQSSMSGGGGG	SGYQCNDDQSGGG 203
		:	:	:	:
QY	85	-QGYQQOQFNQ-----	GGRGNYKNFYNNN	LOGYQ-----	AGPQPSQQGSMLND----- 128
		:	:	:	:
Db	204	GSQGYQQDGRGRG	SGSGGGGGGGG	GYNNRSGGYEPR	GRGGRGGRGGSGDRGFN 263
		:	:	:	:
QY	129	----FOKO-QKOAPKPK	TKLKYSSSGIKLA--	NATKKVGT	KPA-ESDKKEEKSAETK 180
		:	:	:	:
Db	264	KFGVFKKEVYLH	TSPLUKADVL	FQDPTAEWAESL	PFSFTLLSWELEANYEDLOEVLS 323
		:	:	:	:
QY	181	EPTKEPTKVBEPPV	KBEK-----	PVQTEKTEEKS	SELPKVEDLKISETHNTNANV 232
		:	:	:	:
Db	324	SDENGTYVSPPGN	EEESKIFTTDL	PASLAWL	TEERPE--PAEVTSTSQSPHSPD----- 377
		:	:	:	:
QY	233	TSADALIKOE	EEEE 245		
		:	:	:	:
Db	378	SSQSSLAQ	EEEE 390		
		:	:	:	:

RESULT 6
US-08-728-323A-2
Sequence 2A, Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728.323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-728-323A-2

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Query Match
10.8%; Score 145; DB 2; Length 1162;
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[illegible]

RESULT 7
US-09-298-568-2
; Sequence 2, Application US/09298568
; Patent No. 6323792
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballestas, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/298,568
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,422
; EARLIER FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-2

[illegible]

RESULT 8

US-09-410-399-2
; Sequence 2, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Cotter, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; TITLE OF INVENTION: to Genomic Host DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/09/410,399
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-2

Query Match 10.8%; Score 145; DB 4; Length 1162;
Best Local Similarity 22.3%; Pred. No. 0.00047;
Matches 57; Conservative 50; Mismatches 127; Indels 22; Gaps 5;
QY 3 DSNQGNQO--NYQYSQNGNQQGNNRYQGYQVAYNAQAPAGGYQYQGGY 60
DB 608 DEQQDEQQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 665
QY 61 QQYNPDAGYQQQYNPQGGYQQQYNPQGGYQQQYNPQGGYQQQYNPQGGY 120
DB 666 QQDEQQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 725
QY 121 SQGSLNDFQKQQAAPKPKTKLVSSSGIKLANATKVKGTTPAESDKKEEKSAETK 180
DB 726 QDEQQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 770
QY 181 EPTKEPTKVEPVKKEKPV--QTEETKESKELPKVE-DLKISESTHNTNNAVTSADA 237
DB 771 EQQELEDQEQLEEQEQLEEQEQLEEQEQLEEQEQLEEQEQLEEQEQLE 770
QY 181 EPTKEPTKVEPVKKEKPV--QTEETKESKELPKVE-DLKISESTHNTNNAVTSADA 237
DB 771 EQQELEDQEQLEEQEQLEEQEQLEEQEQLEEQEQLEEQEQLEEQEQLE 770
QY 238 LIKEQEBEVDVND 253
DB 831 ELEEQEQLEEQVEE 846

RESULT 9
US-09-894-273-2
; Sequence 2, Application US/09894273
; Patent No. 6756203
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballester, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/894,273
; CURRENT FILING DATE: 2001-06-28
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-2

Query Match 10.8%; Score 145; DB 4; Length 1162;
Best Local Similarity 22.3%; Pred. No. 0.00047;
Matches 57; Conservative 50; Mismatches 127; Indels 22; Gaps 5;
QY 3 DSNQGNQO--NYQYSQNGNQQGNNRYQGYQVAYNAQAPAGGYQYQGGY 60

Db 608 DEQQDEQQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 665
QY 61 QQYNPDAGYQQQYNPQGGYQQQYNPQGGYQQQYNPQGGYQQQYNPQGGY 120
DB 666 QQDEQQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 725
QY 121 SQGSLNDFQKQQAAPKPKTKLVSSSGIKLANATKVKGTTPAESDKKEEKSAETK 180
DB 726 QDEQQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 770
QY 181 EPTKEPTKVEPVKKEKPV--QTEETKESKELPKVE-DLKISESTHNTNNAVTSADA 237
DB 771 EQQELEDQEQLEEQEQLEEQEQLEEQEQLEEQEQLEEQEQLEEQEQLE 770
QY 238 LIKEQEBEVDVND 253
DB 831 ELEEQEQLEEQVEE 846

RESULT 10
US-09-949-016-6646
; Sequence 6646, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6646
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6646

Query Match 10.6%; Score 143.5; DB 4; Length 391;
Best Local Similarity 32.7%; Pred. No. 0.00015;
Matches 51; Conservative 10; Mismatches 58; Indels 37; Gaps 10;
QY 1 MGSNQNQNNQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 49
DB 239 MQQVQGNHMMQRIIPYRPPQQGPPQYSGQEDYQDQYSHGQGGPPEGNNQYYPDG 298
QY 50 QYSGYQGGYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 104
DB 299 NSQYQGGQDAYGGPPQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 352
QY 105 NYNNNQYQAGFQSQSQSLNDFQKQQAAPK 140
DB 353 -----PQQGQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 373

RESULT 11
US-09-949-016-10150
; Sequence 10150, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755


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; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35637
US-09-538-092-1080

Query Match      10.1%; Score 136; DB 4; Length 526;
Best Local Similarity 27.0%; Pred. No. 0.001;
Matches 51; Conservative 9; Mismatches 57; Indels 72; Gaps 10;

QY 4 SNQGNQNYQYQYSONGNGQQ-QGNRYQGY-----QAYNAQAP-----AGGY----- 45
Db 29 SSQPYGQSSYSGYSQSDTDTSGYQSSSYSGYQSONTGYGSTPGYGTGYSQSSSQ 88
QY 46 --YQNYQGYSGY-----QGGYQYVNPDAQYQQYVNPQGG 78
Db 89 SSYQGSYFGYQQPAPSSYSGYSSSSYSGYQPSYQPSYGGQQYGGQ-- 146
QY 79 YQYVNPQGY--QQQFNPQ-----GGRGNY-----KNFNNNNLQ---GYQ 114
Db 147 -QSYNPPQGYQQQYNNSSGGGGGGGGYQDQSSMSGGGGGYGNQDQSGGGGS 205
QY 115 AGFQPSQGG 123
Db 206 GGYQQQDRG 214

RESULT 15
US-09-248-796A-15777
; Sequence 15777, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15777
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15777

Query Match      10.1%; Score 135.5; DB 4; Length 545;
Best Local Similarity 26.0%; Pred. No. 0.0012;
Matches 56; Conservative 25; Mismatches 83; Indels 51; Gaps 11;

QY 3 DSNGQNNQNYQYQYSONGNGQQGNRYQGYQAYNAQAPAGGYQNYQYQYQYQYQ 62
Db 261 DLNDETFFQPYLYLATGFYQQQPFY-----AQ-QPSQQFQYDMF-----GNPI 306
QY 63 YNP-DAGYQQQYVNPQGYQQYVNPQGYQQQFNPQGRGNYKNFNNNNLQYQAGFQPS 121
Db 307 QNPMDTGL---YNOQAYYQQQQQ-QQQQFQP-----NQFTGFNYG----- 344
QY 122 QGMSLNDYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 179
Db 345 -----QPQQPQAPQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 396
QY 180 KEPT--KEPTKVEEPVKEEKPQVTEKTEKSEL 212
Db 397 QQPQFTQPTTA--PLKQNTSSSRFNETHELNDL 429

Search completed: July 1, 2005, 18:39:42
Job time : 20.5994 secs
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```

; Sequence 17107, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 39-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17107
; LENGTH: 741
; TYPE: prt
; ORGANISM: Pichia pinus
US-10-732-923-17107

Query Match      27.8%; Score 374.5; DB 17; Length 741;
Best Local Similarity 37.4%; Pred. No. 1.6e-18;
Matches 105; Conservative 28; Mismatches 85; Indels 63; Gaps 14;

Qy      11  QNYQYQYSONGNOQGNNRYQGYAYNAQAQPAQGYQNYQYGSYQGGYQYQYNPDAGYQ 70
Db      56  QBEQYQGYQGGQQQYNYQ-GGYNNYNNR-----GGYSNNRGGYNNRGGYSYNN---SYN 107

Qy      71  QYNYPQGGYQYQYNPQGGYQQQFNPQGRGNYNKFNYNNN---LQGYQAGF-----QPQSQ 122
Db      108  TNSN-QGGYSYNN-----NNYNNNSYNNNNNNYNNYNNQYNNNSYNNPQGG 151

Qy      123  G-----MSLNDFOKQKQAA-----PKPKTKTLKL-VSSSGIKLANATKKVGTKPAES 168
Db      152  DQQQETGSGQMSLEDYQKQKESLKLNTKPKVKVLKLNLSSTVKAPIVTKKKEEFPVQ 211

Qy      169  DKKEEKSAAE---TKETKTEPTKVVE-----PVKKEKPVQTEKTEKES--EL 212
Db      212  ESKTEEPAKEEIKNOEPAEAENKVEESKVEAPTAAPVSESEFPAST-PKTEAKASKEV 270

Qy      213  PKVEDLKLISSTHTNNANTVSADALIKOEQEEVDVND 253
Db      271  AAAAAALKKEVVSQAKKESNVTNADALVKEQEQIDASIVND 311

```

```

RESULT 6
US-10-732-923-17477
; Sequence 17477, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(532796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 17477
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Yarrowia lipolytica
US-10-732-923-17477

```

```

Query Match      22.3%; Score 300; DB 17; Length 742;
Best Local Similarity 30.5%; Pred. No. 3.5e-13;
Matches 105; Conservative 24; Mismatches 91; Indels 124; Gaps 17;

Qy 1 MSDS-NGG-NNQQYYQYYSQ-NGNQGGNNRYQYQYNNQAQ----- 40
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MSDFNQDFANKANINEQGGGGGGGGQ-----QGYGYQAPQPFVPGQSFVPGQSFVPGQ 56

Qy 41 ----PAGYYQNYQYSGYQ-----GGYQQYQYNP-----DAGYQQQYNP 75
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 57 SFAPOGGYDQ-YQGGGYQYGGYQGGYQGGYQGGNRRGYSGRGGYRGYQGGYNNQYGN 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Qy 76 QGGYQQYNPQGYYQQQFNPPQGG--PGNYKNFNNNLLQGYQAGFPQSQGMSLNDQKQKQ 134
Db 116 QGGYQG--GYQGGYDQNGNQGGYQGGY-----DNQYGYPDPBPBQPKTLTLEEYOKQKQ 168
Qy 135 QAAPKPKK-----TLKLVSSSGIKANATKKVGTKPAAE-----168
Db 169 EALNLKLPKVGGALKITGGDKPKAGGALKIIGDDXPASTCGGALKITGGDPKTSGGALKITGG 228
Qy 169 -----DKKEEKSAETKEPT---KEPTKVEE----PVKBEKPVQTEBKTEEK 209
Db 229 DKPSGGVLKITGGDKSEKKEAVSKEASPAKPESTPKESTPAPASKESTPSAAEKK--EA 286
Qy 210 SELPKVEDLKISESTHNTNNANVTSDALIIEQEHEEVDDVVND 253
Db 287 AE-----NAASADALIAQAENAIQDOETIKE 311

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```

RESULT 7
US-10-437-963-151492
; Sequence 151492, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 151492
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51630C.1.pgp
US-10-437-963-151492

```

Query Match	14.9%;	Score	201.5;	DB	16;	Length	642;		
Best Local Similarity	31.5%;	Pred. No.	3.3e-06;						
Matches	70;	Conservative	28;	Mismatches	89;	Indels	35;	Gaps	10;
Qy	7	GNNQONTQOYSGNGNQOQGNRNYQGYQAYNAQAQAGAGGYQ-NYQGYSGGYQOOGGYQOYNP	65						
Db	438	GNNNGGYQOQRYNGN---NNGRFQOERAVNS---GNGGYRQGGYRGDGGYQOQGRGYSNG	491						
Qy	66	DAGYQ--QOYNPOGGYQO---YNPQGYQOQOQFNPQGGRGNYKNFN-----YNNN	109						
Db	492	NGGYOQOQGYSGNGGYQOQGRGYSNNGGYRR---GGNQGNRNESDSILSPAHPFALTGT	547						
Qy	110	LOGYQAGFQOSQCGMSLNDFOQOQOARAPKPKTKLVLSSSGIKLANA-TKKVGTGTPAES	168						
Db	548	IPATPEKYOQSQSQASSPAPAQOQPQ-----QTLSSSSSSGAAPAPQAQKSAQAPPPAPA	602						
Qy	169	DKKEEKSATKPTKEPTKVEEPFVKCKEKPQVQTEETKES	210						
Db	603	QAKSOAPPAQAK--SOAPAOVKSOAKAPAPAARTKAPSKAQA	642						

RESULT 8
US-09-866-557A-5
; Sequence 5, Application US/09866557A
; Patent No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, S.
; APPLICANT: Hannon, G.
; APPLICANT: Beach, D.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE

; FILE REFERENCE: GNCA-P02-007

; CURRENT APPLICATION NUMBER: US/09/866,557A

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/189,739

; PRIOR FILING DATE: 2000-03-16

; PRIOR APPLICATION NUMBER: 60/243,097

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 1145

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-866-557A-5

Query Match 13.8%; Score 186; DB 9; Length 1145;

Best Local Similarity 33.9%; Pred. No. 8.2e-05;

Matches 58; Conservative 15; Mismatches 54; Indels 44; Gaps 9;

QY 6 QGNNQQ-----NYQQY---SQNGNQOQNNRYQGYQAYNAQAQAPAGGYQNYQGY--- 52

DB 165 QGHHQGRQGQGGYQRRPSGQGGHQQGRQGQGGYQRRPPGQQGHHQGRQGQGG 224

QY 53 -----SGYQGGYQO---YNPDAGYQOQYN--PQGYQO---YNPQGYQOQ---FNPQGGRG 99

DB 225 YQRRPSGQGGHQQGRQGQGGYQRRPSGQGGHQQGRQGQGGYQRRPSGQGGG-- 282

QY 100 NYKNFNNNLQGYQAGFQPSQGMSLNDFQK-----QKQAAAPKP 140

DB 283 -----HQGRQGQGGYQRRPPGQPNQTSQGGYQSRGPPQQAAPLP 327

RESULT 9

US-09-858-862-5

; Sequence 5, Application US/09858862

; Publication No. US20040018999A1

; GENERAL INFORMATION:

; APPLICANT: Hammond, S.

; APPLICANT: Hammon, G.

; APPLICANT: Beach, D.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE

; FILE REFERENCE: GNCA-P01-007

; CURRENT APPLICATION NUMBER: US/09/858,862

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: PCT/US01/08435

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/243,097

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/189,739

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 1145

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-858-862-5

Query Match 13.8%; Score 186; DB 11; Length 1145;

Best Local Similarity 33.9%; Pred. No. 8.2e-05;

Matches 58; Conservative 15; Mismatches 54; Indels 44; Gaps 9;

QY 6 QGNNQQ-----NYQQY---SQNGNQOQNNRYQGYQAYNAQAQAPAGGYQNYQGY--- 52

DB 165 QGHHQGRQGQGGYQRRPSGQGGHQQGRQGQGGYQRRPPGQQGHHQGRQGQGG 224

QY 53 -----SGYQGGYQO---YNPDAGYQOQYN--PQGYQO---YNPQGYQOQ---FNPQGGRG 99

DB 225 YQRRPSGQGGHQQGRQGQGGYQRRPSGQGGHQQGRQGQGGYQRRPSGQGGG-- 282

QY 100 NYKNFNNNLQGYQAGFQPSQGMSLNDFQK-----QKQAAAPKP 140

DB 283 -----HQGRQGQGGYQRRPPGQPNQTSQGGYQSRGPPQQAAPLP 327

DB 283 -----HQGRQGQGGYQRRPPGQPNQTSQGGYQSRGPPQQAAPLP 327

RESULT 10

US-10-055-797-5

; Sequence 5, Application US/10055797

; Publication No. US20030084471A1

; GENERAL INFORMATION:

; APPLICANT: Hammond et al.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE

; FILE REFERENCE: GNCA-P03-007

; CURRENT APPLICATION NUMBER: US/10/055,797

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 60/189,739

; PRIOR FILING DATE: PCT/US01/08435

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 1145

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-10-055-797-5

Query Match 13.8%; Score 186; DB 14; Length 1145;

Best Local Similarity 33.9%; Pred. No. 8.2e-05;

Matches 58; Conservative 15; Mismatches 54; Indels 44; Gaps 9;

QY 6 QGNNQQ-----NYQQY---SQNGNQOQNNRYQGYQAYNAQAQAPAGGYQNYQGY--- 52

DB 165 QGHHQGRQGQGGYQRRPSGQGGHQQGRQGQGGYQRRPPGQQGHHQGRQGQGG 224

QY 53 -----SGYQGGYQO---YNPDAGYQOQYN--PQGYQO---YNPQGYQOQ---FNPQGGRG 99

DB 225 YQRRPSGQGGHQQGRQGQGGYQRRPSGQGGHQQGRQGQGGYQRRPSGQGGG-- 282

QY 100 NYKNFNNNLQGYQAGFQPSQGMSLNDFQK-----QKQAAAPKP 140

DB 283 -----HQGRQGQGGYQRRPPGQPNQTSQGGYQSRGPPQQAAPLP 327

RESULT 11

US-10-350-798-5

; Sequence 5, Application US/10350798

; Publication No. US2004008684A1

; GENERAL INFORMATION:

; APPLICANT: Hammond et al.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE

; FILE REFERENCE: CSHL-P04-010

; CURRENT APPLICATION NUMBER: US/10/350,798

; CURRENT FILING DATE: 2003-01-24

; PRIOR APPLICATION NUMBER: 10/055,797

; PRIOR FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 09/866,557

; PRIOR FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: 09/858,862

; PRIOR FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: PCT/US01/08435

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/243,097

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/189,739

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5

; LENGTH: 1145

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-10-350-798-5

Query Match 13.8%; Score 186; DB 15; Length 1145;

Best Local Similarity 33.9%; Pred. No. 8.2e-05;

Matches 58; Conservative 15; Mismatches 54; Indels 44; Gaps 9;

QY 6 GGNNOQ-----NYQY-----SONGQGNRRYQGYQAYNAQAQAGGYQYQYQY--- 52
Db 165 QGHHQGRGQGGGQGRPSGQGGHGHQGRGQGGGQGRPPGQGGHGHQGRGQGGG 224
QY 53 -----SGYQGGGYQ--YNPDAGYQOQYN--PQGGYQ--YNPQGGYQOQ--FNPQGGRG 99
Db 225 YQRPSSGQGGHGHQGRGQGGGQGRPSGQGGHGHQGRGQGGGQGRPSGQGGG-- 282
QY 100 NYKNFNNNLQGYAGGQPOQSGMSLNDQK-----QYQAAAPKP 140
Db 283 -----HQGRGQGGGQGRPPGQGPQNTQSGQYQSRGPPQGGQAAAPLP 327

RESULT 12

US-10-282-122A-47274
; Sequence 47274, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47274
; LENGTH: 882
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi

US-10-282-122A-47274

Query Match 13.5%; Score 182.5; DB 15; Length 882;
Best Local Similarity 27.0%; Pred. No. 0.00011;
Matches 80; Conservative 41; Mismatches 112; Indels 63; Gaps 15;
QY 2 SDSNQ-----NNQYQYQSN-----GNQGGNNRYQGYQAYNAQAQAGGYQYQYQY 52
Db 38 NDSNSFVLDHNNKAEYSQSDNETGGYSQNRDNRAGYS--QNRDNRAGYSQNRDNR 95
QY 53 S-GYQO-----GGYQYQ--NPDAGYQOQYNPQGGYQ--YNPQGGY-QQGFNPQGG--- 97

Db 96 TGGYSQNRDNRGTGGYSQNRDNRGTGGYSQNRDNRGTGGYSQNRDNRGTGGYSQ 155
QY 98 -----RGYKKNFNNNLQGYAGGQPOQSGMSLNDQK-----QYQAAAPKP 145
Db 156 NRDNRTGGYSQ--NRDNRTGGYSQNRDNRGTGGYSQNRDNRGTGGYSQNRDNRGTGGYSQ 214
QY 146 -----LVSSSGIKLANATKTKVCTKPAESDKKEE--KSAETKEPTKE 185
Db 215 YTTTSMSPRLIKTKVPAIVSSTPAADSENSKELNKLGEKKKQOQESQSKYKTKKAETE 274
QY 186 PTKVEEPVKKEEKPVQTEKTEKSELKPKVDLKISETHN--TNNANVTSDALIK 240
Db 275 SKTIEQKVFEQ---LQKKRENLANPIKSIDIMSGSIITVSDLARKMNLKSSDLIAK 327

RESULT 13

US-10-320-797-3284

; Sequence 3284, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Broshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3284
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3284

Query Match 12.5%; Score 169; DB 15; Length 720;
Best Local Similarity 26.0%; Pred. No. 0.0008;
Matches 64; Conservative 22; Mismatches 80; Indels 80; Gaps 11;

QY 38 QAQAGGYQYQYQGYQOQYQOQYQOQYQOQYQOQYQOQYQOQYQOQYQOQYQOQYQ 97
Db 48 QQQPFDPY-----GQQQGGYPQYQ-----QYQOQGGYPQYQOQYQOQYQOQYQOQYQ 86
QY 98 RGNYNFNNNLQGYQA-----GQFQSQSGMSLNDQKQKQAAAPKPKTKLTVS 148
Db 87 -----QGYVPVGPAGAGPRAYQP--PQARNVQGFQPPSFSSPAPPPTKAPA 132
QY 149 SSGIKLA-----NATKKVGTKPAESDKKEEKSATKEPTKVEEPVKKEE---KPVQ 201
Db 133 GKPVSLSISGGGAPK---AAPLSLSIEKESKSSPKPAAPTTPKPAAPAAKSEASAPVS 189
QY 202 TEETKEEKSELKPKVEDLK-----ISESTHTNNANVT-----AD 236
Db 190 AAEKAEKA-VPLTSDAQGKVVAETSAAKSGASTPVATVSTSTTTFKSVSAKNDAB 248
QY 237 ALIKEQ 242
Db 249 AIYREQ 254

RESULT 14

US-10-732-923-8692

; Sequence 8692, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10

Search completed: July 1, 2005, 18:44:21
Job time : 67.5287 secs

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RESULT 15
US-10-437-963-109378
; Sequence 109378, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109378
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13541C.1.pep
US-10-437-963-109378

```

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2005, 18:06:15 ; Search time 14.7842 Seconds
(without alignments)
1646.548 Million cell updates/sec

Title: US-09-591-632-2_COPY_1_253

Perfect score: 1348

Sequence: 1 MSDSNQGNQNYQYQSQNG.....SADALIKEBEVDVVDVND 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1348	100.0	685	1 EFBYS2	suppressor 2 prote
2	374.5	27.8	741	2 S12921	suppressor 2 prote
3	182.5	13.5	882	2 H70199	translation initia
4	171	12.7	729	2 T51896	probable translati
5	170.5	12.6	456	2 F84993	protein F57B9.9 [i
6	168.5	12.5	405	2 S19355	hypothetical prote
7	168.5	12.5	798	2 T33022	hypothetical prote
8	166	12.3	372	2 I64223	bifunctional endo-
9	163.5	12.1	589	2 S71954	RNA/ssDNA-binding
10	163.5	12.1	1094	2 S49313	protein kinase - s
11	161.5	12.0	3498	2 T22330	hypothetical prote
12	159.5	11.8	1655	2 T13998	gene mastermind pr
13	156	11.6	232	2 T21735	hypothetical prote
14	155.5	11.5	2957	2 T33152	hypothetical prote
15	153.5	11.4	409	2 T20847	hypothetical prote
16	153.5	11.4	1125	2 E90598	membrane nuclease,
17	153	11.4	462	1 LUD07	annexin VII - slim
18	153	11.4	952	2 S64473	translation initia
19	152	11.3	940	2 D89723	protein F39D8.1b [
20	152	11.3	945	2 T21998	hypothetical prote
21	151	11.2	1844	2 D71612	hypothetical prote
22	150.5	11.2	914	2 B48086	translation initia
23	150.5	11.2	1161	2 T18400	glutamate-cysteine
24	150.5	11.2	1390	2 T14004	trfA protein - eli
25	150	11.1	461	2 T10265	arabinogalactan-pr
26	149	11.1	765	2 T15447	hypothetical prote
27	148.5	11.0	867	2 T27136	hypothetical prote
28	148.5	11.0	871	2 T27135	hypothetical prote
29	148.5	11.0	1156	2 T23748	hypothetical prote

30	148	11.0	419	2	T04886
31	147.5	10.9	352	2	T24389
32	147	10.9	597	2	T51889
33	146.5	10.9	462	4	S33798
34	146.5	10.9	665	2	S70706
35	146.5	10.9	800	2	I51653
36	145	10.8	1111	2	T29070
37	144.5	10.7	738	2	S37876
38	144.5	10.7	1004	2	H88562
39	144.5	10.7	1044	2	S40704
40	143.5	10.6	404	2	S46269
41	143.5	10.6	1500	2	T03824
42	142.5	10.6	284	2	T23158
43	142	10.5	676	2	S41022
44	140.5	10.4	236	2	T18240
45	140.5	10.4	870	2	T30110

ALIGNMENTS

RESULT 1

EFBYS2

suppressor 2 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: Gl-to-S transition protein; protein YD9395.05; protein YDR172w

C;Species: Saccharomyces cerevisiae

C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004

C;Accession: S00733; JT0323; S49768; S00488; A26742; S00533; S05723

R;Wilson, P.G.; Culbertson, M.R.

J. Mol. Biol. 199, 559-573, 1988

A;Title: SUP12 suppressor protein of yeast. A fusion protein related to the EF-1 family

A;Reference number: S00733; MUID:8817503; PMID:3280807

A;Accession: S00733

A;Molecule type: DNA

A;Residues: 1-685 <WIL>

A;Cross-references: UNIPROT:P05453; EMBL:X07163; NID:G4581; PIDN:CAA30155.1; PID:G4582

R;Kushnirov, V.V.; Ter-Avanesyan, M.D.; Telchov, M.V.; Surguchov, A.P.; Smirnov, V.N.; I

Gene 66, 45-54, 1988

A;Title: Nucleotide sequence of the SUP2(SUP35) gene of Saccharomyces cerevisiae.

A;Reference number: JT0323; MUID:88329727; PMID:3047009

A;Accession: JT0323

A;Molecule type: DNA

A;Residues: 1-685 <KUS>

A;Cross-references: EMBL:M21129; NID:G172789; PIDN:AAA35133.1; PID:G172791

R;Murphy, L.; Harris, D.E.

submitted to the EMBL Data Library, November 1994

A;Reference number: S49768

A;Accession: S49768

A;Molecule type: DNA

A;Residues: 1-685 <MUR>

A;Cross-references: EMBL:Z46727; NID:G1289283; PIDN:CAA86677.1; PID:G1289287; GSPDB:GN00

R;Kikuchi, Y.; Shimatake, H.; Kikuchi, A.

EMBO J. 7, 1175-1182, 1988

A;Title: A yeast gene required for the Gl-to-S transition encodes a protein containing a

A;Reference number: S00488; MUID:88296422; PMID:2841115

A;Accession: S00488

A;Molecule type: DNA

A;Residues: 1-52, 'C', 54-685 <KIK>

A;Cross-references: GB:Y00829; EMBL:Y00829; NID:G3711; PIDN:CAA68760.1; PID:G3712

C;Genetic8:

A;Gene: SGD:SUP35; SUP12; GST1; SUP2; MIPS:YDR172w

A;Cross-references: SGD:S0002579; MIPS:YDR172w

A;Map position: 4R

C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology

C;Keywords: duplication; GTP binding; nucleotide binding; P-loop; phosphoprotein; tandem

F;1-123/Domain: A <DOM1>

F;42-119/Region: 10-residue repeats

F;124-253/Domain: charged <DOM2>

F;159-222/Region: glutamic acid/lysine-rich

F;254-685/Domain: C <DOM4>

F;261-409/Domain: translation elongation factor Tu homology <ETU>

F;267-274/Region: nucleotide-binding motif A (P-loop)

F;406-409/Region: GTP-binding NKXD motif

A; Introns: 111/1; 711/3
C; Superfamily: suppressor 2 protein; translation elongation factor Tu homology

Query Match 12.7%; Score 171; DB 2; Length 729;
Best Local Similarity 28.5%; Pred. No. 0.0073;
Matches 85; Conservative 23; Mismatches 130; Indels 60; Gaps 13;

Qy 7 GNNOQNYQ-----QYSGNQNGOQGNNRYYGQYAYNA----- 37
Db 3 GNVOQNNEEAAODERLARQTQQOMNINAGTFR-PGAFAFTPGAPSTFGQAAPGETPQ 61

Qy 38 -QAQPAGGYQNY-QGYSGYQGGYGQVNPDPAGYQQQYNPQGGYQQYNPQGGYQQQNFNPQ 95
Db 62 YQQYHYGGAQQGYGGYPQYQGYGQYNNQ--QQQYGAVYGGQYNGYGGQQQQQQQ 119

Qy 96 GGRGNV-KNFNYYNNNLQYQAGFOPQSQGMSLND---FQKQKQKAAPK----PKKTL--- 144
Db 120 QQYGGYQQNGYQQRQQONRDAPKPAQIVKRPEQPAQAQPKADAPKTAAPVPKVLSVG 179

Qy 145 -----KLVSSEGIKANATKV-----GTKPASDKKEEKSAETKEPTKVEEPVKKE 196
Db 180 GDAPAKVLISIGDDAPKPAAKVLISGTAPA---KEEPKKEAAKKEGTAEAAAkvTATKAV 236

Qy 197 EKPVTREKTEKSELPKVEDLKISESTHTNTNNAVTSADALIKE-OEEEVDDDEVND 253
Db 237 QK-----TESAASAGRTSPAPSSGRASPAAKSGNKVSRDVADEKDIOADVDEDTLKE 291

RESULT 5
F88493
protein F57B9.9 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: F88493
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A; Accession: F88493
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-456 <STO>
A; Cross-references: UNIPROT:Q20936; GB:chr_III; PIDN:AAA21172.1; PID:G532820; GSPDB:GNOC
C; Genetics:
A; Map position: 3

Query Match	12.6%;	Score 170.5;	DB 2;	Length 456;
Best Local Similarity	27.0%;	Pred. No. 0.0048;		
Matches	67;	Conservative 30;	Mismatches 102;	Indels 49; Gaps 13;
Qy	13	YQYVSONGNCGGNNRQGYQAYNAQAQAPAGGYQNYQGYSGYQGGYQOYNPDAGYQQQ	72	
Db	97	YAFVPGGYQQQ---NNFQQYGYGPGQQGQNYNNNNNGY-----YNQQ---QQQ	144	
Qy	73	YNPGGY-QQYNPGGYQQQFNPGCGRGNYNFNNNNLQGYAGFGPQCGGSLNDFQK	131	
Db	145	FN-----GYNNYNNNNNQQQPY-NNNNNNYNNNNNNN-----NNYNQQPQG--AQGPQQ	193	
Qy	132	QQQAQPKPKTKLLVSSSGIKLANATKGVGTKPAESDKKEEKSAAETKEPTKVEE	191	
Db	194	QVQQVQQPQGPVQGPQPTPIR-PPQPSRQQPVQS-----FESHTQIVQPVRAVQANAQ	248	
Qy	192	PVKKEKP-----VQTEETEEKSELPKVEDLKISETHTNNNANTVSADALIKEQ	242	
Db	249	LVQPVIRPAASAVATAVVDTSSAKKATEFNKANGIEQPKPAH---AEKASLDA-----	299	
Qy	243	EEEVDDDEV	250	
Db	300	--EVDANV	305	

RESULT 6

S1935S
hypothetical protein YCL028w - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein YCL181
C;Species: *Saccharomyces cerevisiae*
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
A;Accession: S1935S; S17471; C27061
R:Hollenberg, C.P.; Kleinhaus, U.; Lutzenkirchen, K.; Ramezani Rad, M.; Xu, G.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19350
A;Accession: S19355
A:Molecule type: DNA
A:Residues: 1-405 <HOI>
A;Cross-references: UNIPROT:P25367; EMBL:X59720; NID:g1907116; PIDN:C AAA2357.1; PID:e26'A
F:Ramezani Rad, M.; Lutzenkirchen, K.; Xu, G.; Kleinhaus, U.; Hollenberg, C.P.
Yeast 7, 533-538, 1991
A;Title: The complete sequence of a 11,953 bp fragment from ClG on chromosome III encom
A;Reference number: S17471; MUID:g1377317; PMID:1897318
A;Accession: S17471
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-186 <RAM>
A;Cross-references: EMBL:S58084
R:Trueheart, J.; Boeke, J.D.; Fink, G.R.
Mol. Cell. Biol. 7, 2316-2328, 1987
A;Title: Two genes required for cell fusion during yeast conjugation: evidence for a phr
A;Reference number: A93093; MUID:87286864; PMID:3302672
A;Accession: C27061
A:Molecule type: DNA
A:Residues: 1-180,'T',182-322,'VHSQLWLPQVPWTAITPIQIRVMGASNRMLMSMYDRN','RMVNSNPMTSDRTNTA'
A;Cross-references: EMBL:M16717; NID:g171534; PIDN:A AA34615.1; PID:g171536
C;Genetics:
A;Gene: SGD:RNQ1
A;Cross-references: SGD:S0000533
A;Map position: 3L

Query Match	Best Local Similarity	Matches	Score	DB 2;	Length	Gaps
12.5%;	33.3%;	57;	Pred. No.	0.0055;	405;	10;
Conservative	10;	Mismatches	49;	Indels	55;	

Qy 2 SDSNGNQNNQQYYQQYSQNQGNOGNRRYQGYQAYNAQAAGGGYQNYQYSG----- 54
:: :: ||||| |
D b 219 NNQSNNSQGYNQSYQNGNS----QGYN--NQOYGNGGYQQOQOGSGGAFFSLA 271
:: :: ||||| |
Q y 55 -----YQGGYQYNPDAGYQQQYNNPQG--GYQQYNPQG-----GYQQQFNPGQ--- 96
:: :: ||||| |
D b 272 SMAQSYLEGGGTQSN-----QQQYNQQGNMQQYQQOQQYQHQQGGQQQQ---QGHSS 323
:: :: ||||| |
Q y 97 -----GRGNYKNFYNNLNQYQAGFPQPSQG-MSLNDLFKQKQ 133
:: :: ||||| |
D b 324 SFSAALASMASSYLGNNSNSSSYGGQQQANEYG-RPOHQNGQQSQNEVGPRPQ 373
:: :: ||||| |

RESULT 7

T33022
hypothetical protein K07H8.10 - Caenorhabditis elegans
C;Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33022
R:Fulton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, G.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid K07H8.
A;Reference number: Z21264
A;Accession: T33022
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A:Residues: 1-798 <FUL>
A;Cross-references: UNIPROT:O45181; EMBL:AF047659; PIDN:AAC04430.1; GSPPDB:GN00022; CESP
A;Experimental source: strain Bristol NZ; clone K07H8
C;Genetics:
A;Gene: CESP:K07H8.10
A;Map position: 4

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: July 1, 2005, 18:05:25 ; Search time 40.2988 Seconds
(without alignments)
3214.888 Million cell updates/sec

Title: US-09-591-632-2_COPY_1_253
Perfect score: 1348
Sequence: 1 MSDSNQGNQNYQQYSQNG.....SADALIKEBEVDDEVND 253

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1348	100.0	685 1	ERF2_YEAST P05453 saccharomyc
2	1348	100.0	685 2	Q9HGV1 saccharomyc RN
3	1341	99.5	685 2	Q8TFB8 saccharomyc RX
4	1339	99.3	251 2	Q95TM0 saccharomyc RX
5	1339	99.3	429 2	Q96UJ2 saccharomyc RA
6	1332	98.8	251 2	Q96TL8 saccharomyc RA
7	1332	98.8	429 2	Q96TJ4 saccharomyc RT
8	1332	98.8	429 2	Q96UJ0 saccharomyc RL
9	1328	98.5	429 2	Q96UJ9 saccharomyc RL
10	1327	98.4	251 2	Q96UJ5 saccharomyc RN
11	1322	98.1	429 2	Q96UJ1 saccharomyc RP
12	1314	97.5	429 2	Q96UJ8 saccharomyc RX
13	1312	97.3	251 2	Q96UJ6 saccharomyc RX
14	1312	97.3	251 2	Q96UJ7 saccharomyc RT
15	1312	97.3	435 2	Q6Q7I3 saccharomyc RL
16	1308	97.0	251 2	Q96UJ8 saccharomyc RN
17	1308	97.0	429 2	Q96TQ9 saccharomyc RP
18	1305	96.8	435 2	Q6Q7I6 saccharomyc RX
19	1303	96.7	251 2	Q96UJ4 saccharomyc RX
20	1296	96.1	435 2	Q6Q7I2 saccharomyc RA
21	1290	95.7	435 2	Q6Q7I4 saccharomyc RT
22	1285	95.3	242 2	Q8TFR4 saccharomyc RT
23	1281	95.0	435 2	Q6Q7I1 saccharomyc RL
24	1279	94.9	243 2	Q8TFR3 saccharomyc RN
25	1275	94.6	240 2	Q8TFR0 saccharomyc RP
26	1262	93.6	237 2	Q8TFQ8 saccharomyc RC
27	1258	93.3	236 2	Q8TFQ9 saccharomyc RA
28	1241	92.1	235 2	Q8TFR1 saccharomyc RA
29	1240	92.0	233 2	Q8TFQ9 saccharomyc RA
30	1209.5	89.7	666 2	Q8TFR7 saccharomyc RA
31	1209.5	89.7	666 2	Q8TFR8 saccharomyc RA

32	1187	88.1	434	2	Q96UJ3	Q96UJ3 saccharomyc
33	1172.5	87.0	227	2	Q8TFR5	Q8TFR5 saccharomyc
34	1120.5	83.1	216	2	Q8TFR2	Q8TFR2 saccharomyc
35	701	52.0	123	2	Q8TFR6	Q8TFR6 saccharomyc
36	700	51.9	224	2	Q07089	Q07089 saccharomyc
37	686	50.9	120	2	Q8TFR9	Q8TFR9 saccharomyc
38	539.5	40.0	688	2	Q6FVM2	Q6FVM2 candida gla
39	500.5	37.1	662	2	Q9HGI4	Q9HGI4 zygoscacchar
40	483	35.8	299	2	Q9UVK3	Q9UVK3 candida alb
41	483	35.8	715	1	ERF2_CANAL	013354 candida alb
42	475	35.2	274	2	Q9UVJ9	Q9UVJ9 zygoscacchar
43	471.5	35.0	712	2	Q9HGI7	Q9HGI7 candida mal
44	456	33.8	691	2	Q750T4	Q750T4 ashbya goss
45	452	33.5	428	2	Q9URS3	Q9URS3 kluyveromyc

ALIGNMENTS

RESULT 1
ERF2_YEAST
ID ERF2_YEAST STANDARD; PRT; 685 AA.
AC P05453; P05420;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
DE (Translation release factor 3) (ERF3) (ERF-3) (Omnipotent suppressor
DE protein 2) (GI to S phase transition protein 1).
GN Name=SUP35; Synonyms=GST1, PNM2, SAL3, SUP12, SUP2;
GN OrderedLocusNames=YDR172W; ORFNames=YD9395.05;
OS Saccharomycetes cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI TaxID=4932;
RN [1]_TaxID=4932;
RP SEQUENCE FROM N.A.
RX MEDLINE=88329727; PubMed=3047009; DOI=10.1016/0378-1119(88)90223-5;
RA Kushnirov V.V., Ter-Avanesyan M.D., Telckov M.V., Surguchov A.P.,
RA Smirnov V.N., Inge-Vechtomov S.G.;
RT "Nucleotide sequence of the SUP2 (SUP35) gene of Saccharomycetes
RT cerevisiae.";
RL Gene 66:45-54(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87219095; PubMed=3556215; DOI=10.1016/0014-5793(87)80157-6;
RA Kushnirov V.V., Ter-Avanesyan M.D., Surguchov A.P., Smirnov V.N.,
RA Inge-Vechtomov S.G.;
RT "Localization of possible functional domains in sup2 gene product of
RT the yeast Saccharomycetes cerevisiae.";
RL FEBS Lett. 215:257-260(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88172503; PubMed=3280807;
RA Wilson P.G., Culbertson M.R.;
RT "SUP12 suppressor protein of yeast. A fusion protein related to the
RT EF-1 family of elongation factors.";
RL J. Mol. Biol. 199:559-573(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296422; PubMed=2841115;
RA Kukuchi Y., Shimatake H., Kikuchi A.;
RT "A yeast gene required for the G1-to-S transition encodes a protein
RT containing an A-kinase target site and GTPase domain.";
RL EMBO J. 7:1175-1182(1988).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RX MEDLINE=97313263; PubMed=9169867;
RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Ballesta J.P.G.,
RA Bagues M., Baron L., Becker A., Bateau N., Bloeker H., Blugeon C.,
RA Boskovic J., Brandt P., Brueckner M., Buitrago M.J., Coster F.,
RA Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,

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RESULT 5	ID Q96UJ2	PRELIMINARY;	PRT; 429 AA.				
AC Q96UJ2,	Q96UJ2,						
DT DT	01-DEC-2001 (TrEMBLrel. 19, Created)						
DT DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)						
DT DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)						
DE Sup35p (Fragment).	Name=Sup35;						
OS Saccharomyces cerevisiae (Baker's yeast).	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;						
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.	NCB TaxID=4932;						
OX NCB TaxID=4932;	[1]						
RN RN	SEQUENCE FROM N.A.						
RP RC	STRAIN=SLI1010-1A;						
RC RX	MEDLINE=21518585; PubMed=11606520;						
RA RA	Jensen M.A., True H.L., Chernoff Y.O., Lindquist S.;						
RT RT	"Molecular population genetics and evolution of a prion-like protein						
RL RL	in Saccharomyces cerevisiae.";						
DR DR	Genetics 159:527-535(2001). EMBL; AY052613; AAL15028.1; ..						
DR DR	GO; GO:0005525; P:GTP binding; IEA..						
DR DR	GO; GO:0003747; P:translation release factor activity; IEA.						
DR DR	GO; GO:0006412; P:protein biosynthesis; IEA.						
DR DR	GO; GO:0006415; P:translational termination; IEA.						
DR DR	IceterPro; IPR003285; ProTSyn GTPbind.						
DR DR	Ffam; PF00009; GTP EFtu; 1_						
DR DR	PRINTS; PR00315; ELONGATNFCT.						
DR DR	PROSITE; PS00301; EPACTOR_GTP; UNKNOWN_1.						
KW KWP	GTP-binding; Protein biosynthesis.						
FT FT	NON TER 1						
FT FT	NON TER 429						
SQ SQ	SEQUENCE 429 AA; 48238 MW; BAECBCBD6BEA3B2 CRC64;						
Query Match	99.3%; Score 1339; DB 2; Length 429;						
Best Local Similarity	100.0%; Pred. No. 1.6e-65;						
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY 3 DSNQGNNQQNYQVYSNGNQOQGNRRYGQAAYNAQAAPAGGYQNYQGSYGGYYQQ 62							
Dd 1 DSNQGNNQQNYQVYSNGNQOQGNRRYGQAAYNAQAAPAGGYQNYQGSYGGYYQQ 60							
QY 63 YNPdagYQQYNPqgggYqqINpqggyQQFNpqgrgnYKfNyfnnnLNQyqaGFqpQSQ 122							
Dd 61 YNPdagYQQYNPqgggYqqINpqggyQQFNpqgrgnYKfNyfnnnLNQyqaGFqpQSQ 120							
QY 123 GMSLNDfqoKoAQApkPKtKLvSSSGTKLANAtKVGTkpAESDKKEEKSAETKEP 182							
Dd 121 GMSLNDfqoKoAQApkPKtKLvSSSGTKLANAtKVGTkpAESDKKEEKSAETKEP 180							
QY 183 TKExPTkvEEpvKKEEKPVQTeeTKeSkELPkVEDLKISEStHTnNVNTSadAlIKEQ 242							
Dd 181 TKExPTkvEEpvKKEEKPVQTeeTKeSkELPkVEDLKISEStHTnNVNTSadAlIKEQ 240							
QY 243 EEVDVVND 253							
Dd 241 EEVDVVND 251							
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RESULT 6	ID Q96TL8	PRELIMINARY;	PRT; 251 AA.				
AC Q96TL8;	Q96TL8;						
DT DT	01-DEC-2001 (TrEMBLrel. 19, Created)						
DT DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)						
DT DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)						
DE Sup35D (Fragment).	Name=Sup35;						
OS Saccharomyces cerevisiae (Baker's yeast).							
CN GN							


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DR GO: 0005525; P: GTP binding; IEA.
DR GO: 0003747; P: translation release factor activity; IEA.
DR GO: 0006412; P: protein biosynthesis; IEA.
DR GO: 0006415; P: translational termination; IEA.
DR InterPro: IPR00795; ProtSyn_GTPbind.
DR Pfam: PF00009; GTP_EFTU; 1.
DR PRINTS: PR00315; ELONGATNCT.
DR PROSITE: PS00301; EFATOR_GTP; UNKNOWN_1.
KW GTP-binding; Protein biosynthesis.
FT NON_TER 1
FT NON_TER 429
SQ SEQUENCE 429 AA; 48337 MW; 5D72CE3451FD38B9 CRC64;

Query Match 97.5%; Score 1314; DB 2; Length 429;
Best Local Similarity 98.4%; Pred. No. 3.7e-64;
Matches 247; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DSNQGNNOOYQOYSGNGNOQGNRYQGYQAYNAQAOPAGGYQYQYSGYQGGYQQ 62
Db 1 DSNQGNNOOYQOYSGNGNOQGNRYQGYQAYNAQAOPGGGYQYQYSGYQGGYQQ 60

Qy 63 YNPDAGYOOOYNPOGGYQOYNPOGGYQOQFNPQGGRGNYKNFNYNNNLQGYQAGFQPOSQ 122
Db 61 YNPDAGYOOOYNPOGGYQOYNPOGGYQOQFNPQGGRGNYKNFNYNNNLQGYQAGFQPOSQ 120

Qy 123 GMSLNDFOKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSATKEP 182
Db 121 GMSLNDFOKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSATKEP 180

Qy 183 TKEPTKVEEPVKKEKPVQTEKTEKSELKPKVEDLKISESTHTNNANVTSADALIKEQ 242
Db 181 TKEPTKVEEPVKKEKPVQTEKTEKSELKPKVEDLKISESTHTNNANVTSADALIKEQ 240

Qy 243 EEEVDDEVND 253
Db 241 EEEVDDEVND 251

RESULT 14
Q96UJ7 PRELIMINARY; PRT; 251 AA.
AC Q96UJ7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Sup35p (Fragment).
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_TaxID=4932;
RP SEQUENCE FROM N.A.
RC STRAIN=YJM311;
RX MEDLINE=21518585; PubMed=11606530;
RA Jensen M.A., True H.L., Chernoff Y.O., Lindquist S.;
RT "Molecular population genetics and evolution of a prion-like protein
in Saccharomyces cerevisiae.";
RL Genetics 159:527-535(2001).
DR EMBL; AY052606; AAL15021.1; -.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 28372 MW; D56F94D4811C3A8A CRC64;

Query Match 97.3%; Score 1312; DB 2; Length 251;
Best Local Similarity 98.4%; Pred. No. 2.8e-64;
Matches 247; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DSNQGNNOOYQOYSGNGNOQGNRYQGYQAYNAQAOPAGGYQYQYSGYQGGYQQ 62
Db 1 DSNQGNNOOYQOYSGNGNOQGNRYQGYQAYNAQAOPAGGYQYQYSGYQGGYQQ 60

Qy 63 YNPDAGYOOOYNPOGGYQOYNPOGGYQOQFNPQGGRGNYKNFNYNNNLQGYQAGFQPOSQ 122
Db 61 YNPDAGYOOOYNPOGGYQOYNPOGGYQOQFNPQGGRGNYKNFNYNNNLQGYQAGFQPOSQ 120

Qy 123 GMSLNDFOKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSATKEP 182
Db 121 GMSLNDFOKQQAAPKPKTKLVSSSGIKLANATKKVGTGTPAESDKKEEKSATKEP 180

Qy 183 TKEPTKVEEPVKKEKPVQTEKTEKSELKPKVEDLKISESTHTNNANVTSADALIKEQ 242
Db 181 TKEPTKVEEPVKKEKPVQTEKTEKSELKPKVEDLKISESTHTNNANVTSADALIKEQ 240

Qy 243 EEEVDDEVND 253
Db 241 EEEVDDEVND 251

RESULT 15
Q96UJ7 PRELIMINARY; PRT; 435 AA.
AC Q96UJ7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Sup35p (Fragment).
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_TaxID=4932;
RP SEQUENCE FROM N.A.
RC STRAIN=YJM436;
RX MEDLINE=21518585; PubMed=11606530;
RA Jensen M.A., True H.L., Chernoff Y.O., Lindquist S.;
RT "Molecular population genetics and evolution of a prion-like protein
in Saccharomyces cerevisiae.";
RL Genetics 159:527-535(2001).
DR EMBL; AY052608; AAL15023.1; -.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 28336 MW; 68647C0EA2819998 CRC64;

Query Match 97.3%; Score 1312; DB 2; Length 251;
Best Local Similarity 98.4%; Pred. No. 2.8e-64;
Matches 247; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DSNQGNNOOYQOYSGNGNOQGNRYQGYQAYNAQAOPAGGYQYQYSGYQGGYQQ 62
Db 1 DSNQGNNOOYQOYSGNGNOQGNRYQGYQAYNAQAOPAGGYQYQYSGYQGGYQQ 60
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Translation termination factor SUP35 (Fragment).
GN Name=SUP35;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M22, S288C, and M8;
RX PubMed=15059259;
RA Fay J.C., McCullough H.L., Sniegowski P.D., Eisen M.B.;
RT "Population genetic variation in gene expression is associated with
RT phenotypic variation in Saccharomyces cerevisiae.";
RL Genome Biol. 5:R26-R26(2004).
DR EMBL; AY553987; AAS64328.1; -;
DR EMBL; AY553990; AAS64331.1; -;
DR EMBL; AY553985; AAS64326.1; -;
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003747; F:translation release factor activity; IEA.
DR GO; GO:0006412; F:protein biosynthesis; IEA.
DR GO; GO:0006415; F:translational termination; IEA.
DR InterPro; IPR00795; ProtSyn_GTPbind.
DR PRINTS; PR00315; ELONGATNFT.
DR PRINTS; PR01343; YEASTERF.
DR PROSITE; PS00301; EFACITOR_GTP; UNKNOWN_1.
KW GTP-binding; Protein biosynthesis.
FT NON_TER 1
FT NON_TER 435
SQ SEQUENCE 435 AA; 48968 MW; ED0E85699BB28442 CRC64;

Query Match 97.3%; Score 1312; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 4.8e-64;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NNQNYQYQSQNGNQGNRYQGYQAYNAQAQAGGYQNYQGYQGYQGYQYNPDA 67
DB 1 NNQNYQYQSQNGNQGNRYQGYQAYNAQAQAGGYQNYQGYQGYQGYQYNPDA 60

QY 68 GYQQYNPQGGYQYQYNPQGGYQQQFNPQGGRGYKNFNNNLNQGYQAGFQPSQGMSLN 127
DB 61 GYQQYNPQGGYQYQYNPQGGYQQQFNPQGGRGYKNFNNNLNQGYQAGFQPSQGMSLN 120

QY 128 DFQKQQAAPKPKTKLVSSGKLANATKVTGTPAESDKKEEKSAETKEPTKEPT 187
DB 121 DFQKQQAAPKPKTKLVSSGKLANATKVTGTPAESDKKEEKSAETKEPTKEPT 180

QY 188 KVEFPVKKEKXPQTEETKEKSELPKVEDLKISESTHTNNANVTSDALIKEQEEVD 247
DB 181 KVEFPVKKEKXPQTEETKEKSELPKVEDLKISESTHTNNANVTSDALIKEQEEVD 240

QY 248 DEVVND 253
DB 241 DEVVND 246

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